

THE UNIVERSITY OF CHICAGO

ATCTGACCACTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGAGCAGCAGCGCCGCGAGGACCTGGAGCTCCGCTCGCTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGTCTCTGCGCTTCTGTGTG
CTGCTGCCGCCCGCGCCGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCGCGGGGCT
GGTGGACAAGTTTAAACAGGGGATGTTGGACACCGCAAGAAGAACTTTGGCGCGGGAACA
CGGCTTGGGAGGAAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCTGTGTGCTGTCAGTGTGAAGCAGCAATATCTGACTTATTCGAGTGGTTTT
GTGTGAAGACCTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGAGTGTCTGCGATGC
CAGGGCGGATCCAGAGGCCCTGCGAGCGGGAATGGCCACTGCGCGGAGATGGGACGACAGCA
GGGCGACGGGTCTGCCGTGCCACATGGGTACGAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGCTGCTCGGGCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCTGTGTGGATGTGGAACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTTACAGTGGGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGTGTGGACGAGTGTCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAACTGCTCACTACTCCAGGGGACTACGTCTGTGTGTGCTCCTGACGGCTTCGAAGAAACG
GAAGATGCTGTGTGCCGCGCGAGCGAGTGTGAAGCCAGTAAGAGCAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCGCGACTTACCTTTAAATATTTCAGAAGATGTTC
CGTGGAAAAATGTGGCCTGAGGATGCCGTCTCTGCACTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGTTGTCTTTA
AACAGACTGTATATTTTGATACAGTCTTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTGTTTATTGAGCTTATATGTGTACAAATAAAGCAATAGCA
TCACAAATTTCACAATAAAGCATTTTTTCACTGCATTCTAGTTGTGGTTGTGCCAAATC
ATCAATGTATCTTATCATGTCTGGATCGGGAAATTAATTCGGCGCAGCACCATGGCCTGAAAT
AAGCTCTGAAAGAGGAACCTGGTTAGGTACCTTCTGAGGCGGAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGTTGTGGAAGTCCCGAGCTCCCGCAGGCAGAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLPLLLLLPPAPEAAKKTPCHRCRGLVDKFNQGMVDATAKNFGGNTAWEKTL SKYESSEIRL
LEILEGLCESSDFECNQMLEAQBEHLEAWWLQLKSEYFDLFEWFCVKTLKVCSPGTYPGPDCLACQGGSRPCSG
NGHCSDGDSRGDSCRCRMGYQGPLETDCMDGYFSSLRNETHSICTACDESKTCSGLTNRDCGCEVGWVLDE
GACVDVDECAAEPPFCSAQAQCKNANGSYTCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNIPGSYVCVCPDGFETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCTCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACCGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTTCCCGGACGCGAGGAGGTTCTGAGCAGCATGCGCCGGAGGAGCGCTTC
CCTGCGCGCGCGCTCTGGCTCTGGAGCATCTCTCTGTGCTGTGGCAGCTGCGGGCGGAGGCG
CGGGCGCGCGCAGGAGGAGAGCCCTGTACCTATGGATCGATGCTACCCAGGCAAGATCTCA
TAGGATTTGAAGAAGATATCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAAGGCGAGCAGAGTAATCTTCTATGAATTCCTGTCTTGGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCTTCAACAAGGCA
TCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTGGAAGT
GGATGTGATTGTTATGAATTCGAAGGCAACACCATTTCTCAAACACCTCAAAATGCTATCT
TCTTTAAAAACATGTCAACAAGCTGAGTGCCCAAGGCGGGTGCCGAAAATGGAGGCTTTTGTAA
GAAAGACGCATCTGCGAGTGTCTGTATGGGTTCCACGGACCTCACTGTGAGAAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCTCGGTTTTCTGCATCTGCCACCTG
GATTTCTATGGATGAACTGTGACAAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTTCTACCCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCAACAACCTGTGCAAAATGGAGGTAATGCATTGGTAAAAGCAAATGTAAGTGTT
CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT
GGAACTTGCCATGAACCCAAACAATGCCAATGTCAAGAAGTTGGCATGGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTTTAAGTTACACCAAGTTATAGCCTTTTGTAAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTTACACTTAAAGTATCTGGCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTAAGTTTCTAAGTACGCTCTGTAG
CATGATGGTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATATGTCAATTGA
TCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAATTAACAATGCATTTATGGT
GTCTGGGGCGAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGACGTTAATGTTGAAGTTACAGCATTTTCAAGTTTATGTGCAGATATTTAGAT
GTTTGTATACATTTTAAAAAATGCTCTTAATTTTAAACTCTCAATAACAATATATTTTGACC
TTACCATATATCCAGAGATTCAGTATTAATAAAAAAAAAAATTAACATGTGGTAGTGGCATT
AAACAATATAATATATCTAACAACAATGAATAGGGAATATAATGTATGAACCTTTTGTGAT
TGGCTTGAAGCAATATAATATATTGTAACAAAACACAGCTCTTACCATAAACAATTTTAT
ACTGTTTGTATGTATAAAATAAAGTGCTGCTTTAGTTTTTTGGAAAAAATAAAAAAAAAA
AAAAAATAAAAAAAAAAATAAAGGGCGGCCGCGACTTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTATTATTCAGCTTATAATG

0905348-071301

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMIPAIPVNIHSMNFTWQAAGQAEYFYEFLSRLSDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNITLQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCCKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEEERDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

1005548.071201

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGCGGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACAGGGCCCCAGGAGCCACC**ATG**TGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGGCCGGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGGCCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGCACTTCTGGGCACTTC
TGCCCTCGGCGTGCCACCCCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCCTGGAT**TG**AGGGCATTCTCGCTACCGCCTGGGCACCA
TCCGCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG
GTGCTTCCACAGCCTTCGAGGCCCTCTGAGAAGTGCCCAACCTGATTTCATGAGCCTCTGA
CCAAAGCAACTGTGCAGGCTCCTGGGCTTCTCCACAGAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACATGACGCCCTGTCTGTGCGCCCAAGACCTGCTGTCTTGTGAC
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCTGGTGGTCTCTGCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGGCCACTGCC
CACTGCCCCAAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCTGTCTACCGCCT
CGGCTCCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACGACCAACCGCAGCTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTCGGGCCAACCTCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGCGCTCAATGAGTGCGACATCGAG
AGCTTCGTGCTGGGCGTCTGGGGCCGCTGGGCATGGAGGACATGGGTCTACTGAGGCTG
CGGGCACCGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGGCCCCAATG
GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGCGCGGGGTTCCGCTGACGACGCGCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCCAGACCTCCCACTGGGGACGGGGCAGGGCTTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCCAATACCCACCCCAATCCCGTATTTCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCTCTGGGTTC
AGTGACCTCCCACTCCGCTCTCAAGTAGCTGGGACTACAGGTGCACCAACACACCTGGC
TAATTTTTGTATTTTTTTGTAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC
CTGGGCTCAAGCGGTCCACCTGCCCTCCGCTCCCAAGTGCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCTGATTCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTAAAA
TAAACCAAGTATTGATAAAAAAAA

0990548:071201

060507Z

```
><subunit 1 of 1, 164 aa, 1 stop
```

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEODLCCRGRADDC

CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

amino acids 78-82, 161-165

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

amino acids 26-30, 318-322

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAATGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGTGTCTCCCTGCACTCGGCCTGTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCTCTCTGTGTGCTGTTTC
CATGGCCCAGCATTTCTCCACCCTTAACCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLLDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGFAPSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

TOE720.84ES060

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCCATGCGGAGCCGCCCGCTGCTGCCCAACCTCACTCTGT
GCTTACAGTGTGTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGAGATCGTGCTGGAGAACAATAACGCGCTTCCAGAACGCCCGGCACGAGG
GCTGGTTTACATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCAGGCCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCAACGC
CGAGAAGCAGAAGCAGTTTCAGTTTTGTGGGCTCCGCCCCACCCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTACGTAGTCTGGGAGGCAGGGGCGAGCAGCCCCCTGGGCCGCCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTCCCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAAT
GAGTGTCAACCCTGATCTCAGGCCACCAAGCCTCTGCCGCCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTACGCGACTGAAGGCCCTTGACAGCAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTGTTGTTGTTTTCAGGAAAAAAGAAAGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCTGTC

0905346.07.2024

FIGURE 11

MGAARLLPNLTLCLQLLLCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLE
NNYTAFQNAHEGWFMATPRQGRPRQASRSRQNRQEAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTTCTTTTCCCACCACATTGTATTTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCT
GAAGTCTTGGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGTGCGACAGGAACTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC
TGGATTTCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTACAGATTCTCCATTGTCAGGAAAAC
AATATTACAGCATTTCACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAG
TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
CACCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTGAGGACAACCGAT
AAACCACATCTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTTGTATAATCTCTCCAACCTGGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTTGTGACTGACAGTATAAATGGGTACAGAAATGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTTGAACAAGTCCGGG
GGATGGCCGTGAGGGAATTAATATGAATCTTTGTCTGTCCCAACGACCCCGGGCCTG
CCTCTCTTCAACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCTCTCTAT
TCCAACCCCTAGCAGAAGCTACACGCCCTCCAACCTCTACCATCGAAACTTCCCACGATTC
CTGACTGGGATGGCAGAGAAAGAGTGACCCCCCTATTCTGAACGGATCCAGCTCTCTATC
CATTTTGTAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCAACGTGATGGCATA
CAAACCTCAGATGGTGAATGGGCCACAGTTTAGTAGGGGCATGTTTACAGGAGCGCATAG
TCAGCGGTGAGAAGCAACCTGAGCCTGGTTAACTTAGAGCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTTGTTAGAGGC
CACCAACCATGCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGGCCGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCATCTGGAGATGACAGAAACAGTTTTCAGATCGTCTCCTTAAATAACGAT
CAACTCCTTAAAGGAGATTTAGACTGCAGGCCATTACACCCCAATGGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTGCACATAAAGACACGACGATTACATTGATAAATGTTACACAGATGCAT
TTGTGCAATTGGAATCTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACCTTTTGCTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNDSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTCLKKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDSIKWVTEWLKYPSSSLNVRGFMCGPEQVRGMAVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTT SKLPTIPDWGGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRAVEDTICSEATHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKNRGRKDDYCEAGTKKDNS ILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

090530.07.201

FIGURE 14

ACTTGGAGCAAGCGGCGCGGCGGAGACAGAGGCGAGAGGCAGAAAGCTGGGGCTCCGTCCTCGCCTCCACGAGCG
 ATCCCGGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCGGACGAGGAGAACCCGGGTGGCTGCGCCCTGTCC
 TCGCTTCCGAGGCGCGGCGGCTGCGACCTTGCCTCTTGTCTCGCTTGA~~AAAT~~TGGAAAAGATGCTCGCAGGCT
 GCTTTCTGCTGATCCTCGGACAGATCGCTCCTCCTCGCGAGGCGAGGGAGCGTCGACCTGGGAGGTCATCT
 CTAGGGGCGACACGCTCGGACCCACCCGCGAGACGGCCCTTCTGGAGAGTTCTCTGTGAGAACTCAAGCGGGCAGAC
 TGGTTTTCATCATTTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGTCAAGAGGTTCACTGCGGACA
 TCTTGCAATTCTTGGACATTTGGTCTGTATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
 AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTCTGCAAGAGGATCGCGGCTGTCTCCACGG
 GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTTCAAGAACGAGAGGGGCCCGGCCCTGGA
 GGGAGAAATGTGACCGGCTCAATATGATCGTGACAGATGGGAGACCTCAGGACTCCGCGGGCAGAGTGGCTGCTGA
 AGGCAGCGACACGGGCTCTTAATCTTTGCCATTGCTGTGGGCGAGGTGAGACTTCAACACCTTTGAAGTCCATTG
 GGAGTGAGGCCCATGAGGACCATGTCTTCTTGTGGCCAAATTCAGCCAGATAGAGACGCTGACCTCCGTGTTCC
 AGAAGAAGTTGTGACGGCCCATGTGTCAGCACCTGGAGCATAACTTGCCCACTTCTGCATCAACATCCCTGT
 GCTCATACGTTCTGAGGTGCAAAACAGGCTACATTTCACTCGAGTCAAGACGCTTGCAGAACTCAGGATCTGT
 GTGCGCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCGGGCTCCTTCGCTGCGCAGTGTCTACAGT
 GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACACAGGATGTGAAC
 ATGAGTGTGAATGCTGATGGCTCTTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA
 CGTGCAACCGGATCAACTACTGTGCATGAAACAAACCGGGCTGTGAGCATGAGTGGCTCAACATGGAGGAGAGCT
 ACTACTGCCGTGCCACCGTGGCTCACTCTGACCCCAATGGCAAAACCTGCGACCCGAGTGGACCTGTGCAC
 AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCTGCTGCCAGTGTCTCAGAAGGCTTCC
 TCATCAACGAGGACCTCAAGACTGCTCCCGGGTGGATTACTGCCCTGCTGAGTGCACCATGGTTTGTGAATACTCT
 GTGTCAACATGACAGATCTTGTGGCTCTGGGCGGACACGGTTGTGAACATTCGTGTGAAGCAGTGAAGATTCGTTTGTGT
 GCGAGTGTCTTGAAGGTTATATCTCCGTGAAGATGAAAAAACCTGCAGAAAGAAAGATGTCTGCCAAGCATATAG
 ACCATGGCTGTGAACACATTTGTGTGTGAACAGTGAAGCTCATACAGCTGCGAGTGTGTGGAGGGATTCCGGGCTCG
 CTGAGGATGGGAAACGTCGCGAAGGAAGGATGTCTGCAAAACCAACCCATGGCTGTGCGAACACATTTGTGTGA
 ATATGGGAATTCACATCTGCAAAATGCTCAGAGGGGATTTGTTCTAGCTGAGGACGGAAGACCGGTCAAGAAAT
 GCACTGAAGGCCCAATTTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAGCAACATTTGTGGTGT
 TGAAGCAGTTTGTCACTGGAATATAGATTCTTTGACAAATTTCCCCCAAAGCCGCTCAGAGTGGGGCTGTCTCAGT
 ATTTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACATGAAAAAGGCCGTGGCCC
 ACATGAATATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAAGAGAAGTTTATCCCAAG
 GAGAAGGGGCCAGGCCCTTTCCACAAGGGTGCCAGAGCAGCATTTGTGTCAACGGAAGCGGCTCAGGATG
 ACGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAAGCCATTG
 AGGAGGAATCAAGAGATTTGCTCTGAGGCCACAAACAGCATCTCTTCTATGCGGAAGACTTCAGCACAATGG
 ATGAGATAAGTGA~~AAAA~~AACCAAGAAAGGCACTCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
 CAGGGGAATCGCCAAAAACGCTCCAACAGCCAAACAGAACTGAGCCAGTCAACATAAATATCCAAAGACTACTTT
 CCTGTCTCAATTTTGCAGTGCACAACAGATATCTGTTTGAAGAAGACAATCTTTACGCTCTACACAAAAGCTTT
 CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAAATGTGAAAAACCTTATAATGT
 TCCAGAACTTGC~~AA~~ACGAGAAAGTAA~~AAAA~~ATAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCCC
 TGGAAATCGCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCAATGTATACGGGATTACAGT
 GAACCGCAGTGCAGAGCCCCAAGCTCAGGCTATGTTAAATCAATAATGTTGTGAAGTAAAAACATCAGTACTGA
 GAACACTGTTTGTGCCACAGAAACAGAGATATACACTAACTGTATAAATTTATCTTAGGAAAAAATCTT
 TCAAGATTTCAAGATGAATTTACAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGAATATATCTGTGGACAC
 AACTTGTCTCTGCTCATCTGCTTATGTGTGCAATCTATTGACTATAGATAAAGTTTGCACAGTCTTACTTT
 CTGTAGAACACTGGCCATAGGAATGCTGTTTGTGATCGGACTTACCTTGATATATGATATGATGATGATG
 CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATAAAATTCACCACTTCAG

0605348.07301

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEPIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSKTFKRKSEVERAV
KMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPDSDVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTVSFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCBQLCVNVPGSFVCQCYSGYA
LAEDGKRCAVDYCASENHGCEHECVNADGSYLCQCHGFAINPDEKTCRINICALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPGHHVLRSDGKTCAKLDSALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCBCELEGFRLA
EDGKRCCRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMYMGKGSMTGLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASAKAN
GITMYAVGVGKAIIEELQEIASEPTNKHLYFAEDFSTMDEISEKLKKGICBALEDSDGRQDS
PAGELPKTVQOPTSEPTVINIQDLLSCSNFAVQHRYLFEEEDNLLRSTQKLSHSTKPSGSP
EEKHDKCKCENLIMFQNLANEVVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGCTCTCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGACCCAGCATTAGATGTCTATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCCTGGTTGGACTGGGTTGCTGGCTGGGCTGGTCC
TCTTGTAACCAACGCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCTCAACCAATATCCCCCATCCCTGGTGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTAT**TGAT**GAC
CCCACCACTCATTGGCTAAAGGATTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGAATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGTACTCACCAAGAGTGAGGGGCAGAGACTTCAGTCACTGAGTCTCCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAAATTTAAATAAAGATACATAA
TGTTTGATGAAAAA

304549.071301

FIGURE 18

CGCCACCACCTGCGGCCACCGCCAAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTG
 TTGAATTGTTCCCTATACCTCAAAATTCACCAACAGACACCTTTCTCCCAAATGCCAAATGTGA
 AATACGCAATGGAAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAATGGTGTGCACAA
 TTTGTGAAGATGATAATGAATGTGGAAATTTAACTCAGTCTGTGGCGAAAATGCTAATTGC
 ACTAACACAGAAGAAAGTTATTTATTGTATGTGTGTACTTGCTTCAGATCCAGCAGTAAACCA
 AGACAGGTTTATCAGTAATGATGGAACCGCTCTGTATAGAAAATGTGAATGCAAACTGCCATT
 TAGATAATGTCTGTATAGCTGCAAAATATTAATAAAACTTTAAACAAAATCAGATCCATAAAA
 GAACCTGTGGCTTTGCTACAAGAACTCTATAGAAAATCTGTGACAGATCTTTCACCAACAGA
 TATAATTACATATATAGAAAATTTAGCTGAATCATCTTCACTACTAGGTTACAGAACAACA
 CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAAATTTGTA AAAACCGTGAAT
 AATTTTGGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
 ACATCTTACAAAACCTCATGACACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
 AAAAGACCACAGAGTTTGATACAAATTCACCGGATATAGCTCTCAAAGTTTCTTTTTTGAT
 TCATATAACATGAACATATTTCACTCCTCATATGAATATGGATGGAGACTACATAAATATATT
 TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATA
 AGAGTATTGGTCTTTGCTTTTCATCATCTGACAACCTCTTATTGAACCTCAAAATTTATGAT
 AATCTGAAGAGGAGGAAAGAGTGCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCC
 ACCACATTTATGAACTTGA AAAAATAACATTTACATTAAGTCTATCGAAAGGTCACAGATA
 GGTATAGGAGTCTATGTGCATTTTGGAAATTACTCAGCTGAATACCATGAATGGCAGTCTGTCT
 TCAGAGGGCTGTGAGCTGCATACCTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
 GACACATTTTGCATTTTGATGTCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTC
 TTACAGGATCACTCAACTAGGAATAATTTTCACTGATTGTCTTGCCATATGCATTTTT
 ACCTTCTGGTCTCTCAGTGAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG
 TAGCCTATTTCTTGCTGAACCTGTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCT
 TCTGTTCAATCATGCGGAGCTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGC
 ATTGAAGGCATACATCTCTATCTCATTTGTTGTGGGTGTCATCAACAAGGGATTTTGTGCA
 CAAGAAATTTTATATCTTTGGCTATCTAAGCCAGCCGTGGTAGTTGGATTCTTTGCGCAGCAC
 TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAAACAACCTTTATT
 TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTTGGCTTTTGGAGTCAT
 CATATACAAAGTTTTTCGTCACTGCAGGGTTGAAACAGAAAGTATAGTTGCTTTGAGAAC
 TAAGGTCTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACCTGGATCTTT
 GGGGTTCTCCATGTTGTCACGCATCAGTGGTTACAGCTTACCTTTCACAGTCAGCAATGC
 TTTCCAGGGGATGTTTCAATTTTTTTTATCTCTGTGTGTTTTATCTAGAAAAGTTCAAGAAGAA
 ATTACAGATTGTTCAAAAATGTCCCTGTGTTTTGGATGTTTAAAGGTAACATAGAGAATG
 GTGGATAATTCAACTGCACAAAATAAAAAATTTCAAAGCTGTGGATGACCAATGTATAAAAA
 TGACTCATCAAATTATCCAATTATTAACCTACTAGACAAAAAGTATTTTAAATCAGTTTTTCT
 GTTTATGCTATAGGAACCTGTAGATAATAAGGTA AAAATATGTATCATATAGATATACATATG
 TTTCTATGTGAATAGTTCTGTCAA AAAATAGTATTCAGATATTTGGAAGTAATTTGGTTT
 CTCAGATGATATCACTGCACCCCAAGGAAAGATTTTCTTTCTAACAACGAGAAGTATATGAA
 TGTCCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTGCTTTGAAACTAGTCC
 CCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGAAACATAGAGGAATGAAGGGCAGA
 ATATCAACACAGTGAAAGGGGAATGATAAGATGATTTTGAATGAACCTGTTTTCTGTAGAC
 TAGCTGAGAAATGTTTGACATTA AAAATAAGAAATGAAGAAACACATTTTACCATTTTGTGAA
 TTGTTCTGAACTTAAATGCCACTAAAACAACCTTAGACTTCTGTTTGTCTAAATCTGTTTCTT
 TTTCTAATATTTCAAAAAA AAAAAAGGTTTACCTCCACAAATGAAAAA AAAAAA
 AAAAAA AAAAAA AAAAAA AAAAAA

0905348.07304

FIGURE 19

MKRLPLLVPFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVICAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFEVKTVMNFVQRDFTVVWDKLSVNHRRLTHLTKLMHTVEQATLRISQSFQKITEFDT
NSTDIALKVFFFDSYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLPQONDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSFDTMNGSWSSSEGCETYSNETHHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSEIAGL
LHYFFLAFAWMCIEGIHLVIVGVYINKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIWFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHVASVVTAYLFTVSNAPQGMFIFLFLCVLSRKIQEYERYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

0906348-071303

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAAGTCATCGAAAGTCCAGATAGGTATA
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGCGAGCTGGTCTTCAGAG
GGCTGTGAGCTGCATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTATGATGTCCTCTGGTCCCTCCATTGGTATTAAAGATTATAATATTTCTTCAA
GGATCACTCAATAGGAATAATTTATTCACGATTGTCTTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTTCAAGCACCGAGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCAACCCGGCTGGGA
CAAGAAGCCGCGCCTGCCTGCCCGGGCCCGGGAGGGGGCTGGGGCTGGGGCCCGAGGCCG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGCTTTGGGCACCTACCCGTGGGGCCCGTAAGCGCTACTATATAAGGCTGCCGGCCCGGAG
CCGCGCGCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACCTACGGCTGGGGCGACCCCATCCGCTGCGGCACTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGCTGCTGGACTGCGCGCGGGC
CAGAGCGCGCACAGTTTGTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACAGCGTGGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGTCTCCCTGAGCAGTGCCAAACAGCGGCACTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCCTGCCCATGCTGCCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGGAACTTGACATGTCTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACT
GAGACCATGCCCCGGCCTTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCTGTAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTGTACATATTAGAGTTTTCCATTTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCCTTTGAAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
CTGAGGCCAGTTCTGTATGGATGCTGTCTTGAGAAATAACTTTGCTGTCCCGGTGTCACCTGC
TTCATCTCCAGCCCCCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTTATGTCAACCTGCACCTTCTTGTTCAAAAATCAGGAAAAAGAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTTCCCGCACTTGGTTTTTCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTCTTACATATTTATGCCCCCAATTATATTTATGTATGTAAGTGAGGTTTTG
TTTTGTATATTAATGAGTTTTGTTTTG

0906348.071304

FIGURE 22

MRSGCVVHVHWILAGLWLAVAGRPLAFSDAGPHVHYGWGDP IRLRLHYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLEIKAVALTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFE
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTGCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCAAA
AGACCAACAAGTAGTACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCTCCAGATTAGAGTGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACTGGAAC
TGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCTTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTTCTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAAATCCAGCACTTTTGGAAAG
CCGCGGCGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
CATCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

0905348.071301

09876

Signal peptide:

Transmembrane domain:

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
 AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAAACATGCTCCACAGCCCGGACCTGGCAT
 CATGCTGCTATTCCCTGCAAACTACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
 ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
 TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGACAAATG
 CAATTGTGGCACTGGCAGCTTATTTAGTGAAGAAAAAATTTGTGGTTCTATGGCATTATCA
 TTTGACAAATGCAAGCATCTTCTCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTG
 TGGAATCTTTAAGGGCCCATTAATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
 CCGAATTCATGTGCTACTTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
 TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCCTTGGTTTACACCCAGATCCATTTAT
 ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCCTTTAACTTTCCAGCCAGATTTGCC
 AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
 ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT
 ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACCTTACTGA
 ACTGCCGTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAACTCTATATTAAATCACAAC
 TGCTTTCTACAATTTCACTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
 AATTCAAATAGATTTGCAGATGATCAACAGTAAGTGGTTGTGCTCTTCCAAATCTAGAGAT
 TCTGATGATTGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA
 ATCTTCGCAGCCTGGTTATAGCTGGTATAAAACCTCACAGAAATACAGATAACGCCCTTGGTT
 GGACTGGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
 TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAACTCTATTAATAGAA
 TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCT
 GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
 TACTAACACCCCTAGATTGTCTTACATTCAACCCCAATGCATTTTTCAGACTCCCCAAGCTGG
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
 CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCTCCGTTG
 GATGAACATGAACAAAACCAACATTCGATTCTGGAGCCAGATTTACTGTTTTCGCTGGACC
 CACCTGAATTTCAAGGTGAGAATGTTCCGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT
 CTCCCTCTTATAGCTCCTGAGAGCTTCTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
 TTCCTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
 GTCAAAAATCTTGCCATAATACCTTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
 GATATAAATGGCGTAATCCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT
 TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAAATG
 GCTCTTTGAATATTAATAAAGAGATATTCAAGCCAATTCAGTTTGTGGTCTCTGGAAAGCA
 AGTTTCAAATTTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAAATTTCTCA
 TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
 CATCAACTGAGTATAAAATTTGTATTGATATCCCACCATCTATCAGAAAAACAGAAAAAAA
 TGTGTAAGGTGCACCCCAAAGGTTTGACCCGTATCAAAAAGATATGAAAAGAAATTAATAC
 CACAACAATTTGGCCTGTCTTGGAGGCCTTCTGGGGATTATGGTGTGATATGTCCTTATCA
 GCTGCCCTCTCCAGAAATGAACGTGTGATGGTGGACAGCTATGTGAGGAATTAATCTTACG
 AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
 AGAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCACAATAATGTCTCT
AAAAACACCAAGGAACCTACTCCAAAAATGAAC

0905348.071301

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQIILLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTETPEKCLSELSNLQELYINHLLSTISPGAFICLHNLLRLHLSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESI SFYDNRL
IKVPHVALQKVVNLFKFDLNLKNPINRIIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLDP
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYGTIESLPNLKEISIHNPIC
DCVIRWMNMNKTNI RFMEPDSLFCVDPPEFQGGQNVQRQVHFRDMMEICPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWI TP SGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFAV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

03605348.071304

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCAATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCACTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGITTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACATATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCACTTTTTTTTGAATTATGCCACTGCTGAACCTTTTAAACAACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAACA

15005349.071373

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLC SSSGGLNVTC SNANLKEI PRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF
NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVVYVRQNE DARRHLEYLKS LPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

0905348.073301

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCGAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGGCTGCTGGCAGCCCATCTCTGCTGGTGT
GGGCTCAGTGCTGTGAGCTCGGCCACGGGCTGCCGCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAACCGCTCAACCAGGACGAGTTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCGCTGGAGCCCCGGG
CCTTCAACAACCTCTTCAACCTCCGACGCTGGGTCTCCGACGCAACCCTGAAGTCTATC
CCGCTAGGGCTCTTCACTGGGCTCAGCAACCTGACCAGCAGGACATCAGCGAGAACCAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCTCAACAGCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGAGATCTCCCACTGGGCCCTACTTGGACACCATGACACCCAA
TGCTCTACGGCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGCTCCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCTTCAACCCCATCA
GCACCATGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCGAGCTGGCCGTGGTGGAGCCCTATGCCCTCCGGCGCTCAACTACCTGCAGCTGTCTCAA
TGCTCTTGCAACCGACTGACCACACTGGAGGAATCAGTCTTCCATCGGTGGGCAACCTGG
AGACACTCATCTGGACTTCAACCCGCTGGCCTGCGACTGTGGCTCTGTGGGTGTTCCGG
CGCCGCTGGCGCTCAACTTCAACCGGCAGCAGCCACGTGCCACCGCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACTGCGCCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGCGCACAGGTGCAATTT
GTGTGCCGGGCGGATGGCGACCCGCGCCGCCATCTCTGGCTCTACCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCCAGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACCGCGGCGGCAACGAC
TCCATGCCCGCCACCTGCATGTGCGCAGTACTCGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTTCCTTTCATCTCCAACCGCGGCGAGGAGAGGCCAACAGCACCCGCGCACTG
TGCTTTTCCCTTTCGACATCAAGACCTTATCATCGCCACCACCATGGGCTTATCTCTTTC
CTGGGCGTGTCTCTTCTGCTGTGTGCTGTTTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACAACTCGAGATCGAGTATGTGCCCGGAAAGTCGACCGCAGGATCAGCTCCGCGG
ACGCGCCCCGCAAGTTCAACATGAAGATGATAATGAGGCGGGGGCGGGGGCAGGGACCCCCG
GGCGCGGGCAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCCAGTCTTCCACCTC
CTCCCTACCTTCTACACAGTTCTCTTTCTCCCTCCCGCTCCCTCCCTGCTGCCCCCG
CCAGCCTCACCACCTGCCCTCTTCTACAGGACCTCAGAAGCCCGAGACTGGGACCCCA
CAGTACAGGGGATGACAGACTGGAGTTGAAAGCGCAGCAACGACACGCGGACAGTCA
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAAGTTGGGTTTCAATAATTATGGATTTT
TATGAAAACTTGAAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAA

0905348-071301

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKODISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLSLEQLTLEKCNLTSIPTALSHLHGLIVLRRLHNLINAIIRDYSFKRLYRLKVLEISH
WPYLDTMTNCLYGLNLTSLSIITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLEHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETILDSNPLA
CDCRLLWVFRRRRLNFRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVQDNGTYL
CIAANAGGNDMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLFLWLRGKGNKHNIEIYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCTCCCATCCCCAGCCCCGGGATTTCAGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCGGAAGCGCGATGCGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTG
TGTTCCGCTGCTGCTGGCGCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGTGGTGGCACCCTGGTGTCTAAGTGCCAAAGTAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTGAGTGTGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCCTGT
GCGAACTGCCAAGTCCCCTCGTCACTGTGTAGGAATTCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTGAGTCTTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTGAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTTATTGTCTTCCTGCTG
CTCATCATGTCTATCTTCTTGGCCACTACTTGATCCGGCACAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCTGCCCACTTCTCTGC
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGACGGGCGGCCCTCCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACATCC
CAAAATCAAACTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

0905348.071301

FIGURE 32

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRILQVLTSTPHELISISNVALADEGEYTCISFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHLCEGRGNFVPQQYLWEKEGSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLIIMLIFLGHYLI RHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCTCTGG
 CTTCCGACATTGGAGCACTAAATGAACTTGAATTTGTGCTGTGGCGAGCAGGATGGTCGCTG
 TTACTTTTGTGATGAGATCGGGGATGAATTTGCTCGCTTTAAAAATGCTGTGCTTTGGATTCTGTT
 GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAACGTTACAGGGGACGTTTGCAGGAGAAGA
 TCTGTTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGGCTTCACA
 AGCTCGACGCGTTTCACTGCGCCGACTTCCAGTTTACCATTTTTCTGCATGGCAATTC
 CCTCACTCGACTTTTCCCTAATGAGTTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
 AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTCTGCGGCTGCAGCTGGTGAAAAAGG
 CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
 TCTGGAATATCTCCAGGCTGATTTTAATTTATTAACGAGATATAGACCCGGGGGCTTCCAGG
 ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
 GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAAACAGGCTGAAAAAGCTGCC
 CTATGAGGAGGTCTTGGAGCAAAATCCCTGGTATTGCGGAGATCCTGTAGAGGATAACCCCT
 GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAAACATTTCCCAAGAATGCC
 CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCGAGGTAAAGACCTCAATGAAAC
 CACCGAACAGGACTTGTGCTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGCGCCCCCTG
 CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
 GATCATGGCACACCGAGGTCTGCTCCAACCGGAGGTACAAAGATCCGAGGCAACTTGCAGAT
 CAAAATCAGACCCACAGCGAGTAGCGACGGGTAGCTCAGGAAACAAACCTTAGCTAACA
 GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCCACATCCAGGGTGGGTTTAAAGATGAAC
 TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAGCCCAAGCTCTCTAACGTGCAGGA
 GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAAATCGCACTTTGTGGATTACAAGA
 ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAAACATTTCAAG
 AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTAACCTGGACACGCTGTCCCGGGA
 GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
 TCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAACCTG
 CTGAGGTCCCTGCTGTGGAGTGTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
 CAATTACTTCATGTACTCCCGGTGGCAGGGGTGCTGGACAGTTAACTCCATCATCCAGA
 TAGACCTCCACGGAAACCCCTGGGAGTGCTCTGCAACAATTGTGCTTTCAAGCAGTGGGCA
 GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
 TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
 CGCCACGTTAACTTCGACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGACGCACTCC
 AACTCCTACCTAGACACAGCAGGGGTGCTCATCTCGGTGTTGGTCCCGGACGTGCTCGTGT
 GTTTTGCACCTCCGCTTACCCGTGGTGGGCTGCTCGTGTATTTATCCTGAGGAACCGAAAGC
 GGTCCAAGAGAGAGATGCCCAACTCTCCGCTCCGAGATTAATTCCTTACAGACAGTCTGT
 GACTCTTCTACTGGCAAAATGGGCTTTACAACGAGATGGGGCCACAGAGTGTATGACTG
 TGGCTCTCCTCCTCTCAGACTTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
 ATACATCTTCCCAACCGCAGGCACCCCGGGGGCTGGAGGGCGTGTACCCCAATCCCGCG
 CCATCAGCCTGGATGGGCATTAAGTAGATAAAATAACTGTGAGCTCGCACAAACCGAAGGGCCT
 GACCCTTACTTAGCTCCCTTCTTGAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
 GCCACGTGCTCTTTGTGTAGAGCCCTTTTGACAGAAAGCCGACGACCTGCTGTGAAG
 AACTGACAGTGCCTCCGCCCTCGGCCCCGGGCTGTGGGGTGGATGCCCGGCTTCTATAC
 ATATACATATATACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
 CCCCCTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
 TGTAATAAGTAACCTTGTACTTCTGAC

0090546.07.301

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLEIIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFODLNKLEVLILNDNLISTLPANVFQYVPIIHLDLRG
NRLKTLPIYEEVLLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIKPNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSLLPAPPAQEETFAPGFLPTPFKTNQGEDHATPGSAPNGGK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHI PGSGLKMMNCNNRVSSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPOLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFTSAFTVVGMLVFILNRKRKRDRDANSSASEINSLQTVCDSSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCCTGTACCCGCGCGCAGCTGTGTTCTGTACCCCAAGAATAAAGTACAGGGC
TGACCCGGGCGCTGGCAGCGCTCCGCACACATTTCCTGTGCGCGGCTAAGGGGAAAGTGTGGC
CGCTGGGCGCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCTCAG
AGAAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCGGGCCGGCGG
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCGAGGAGGCGCTGCATCTTGGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCGCCAGG
GCCCGGAGGGGGCTCCAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGCTCCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTCCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACTGTGCAAGTACCAAGTTTGAGGTCTTGTGCTCTGCGCCGCGCCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCAGCTGCACAGCGCGCTCTGAGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTTGCA
TCGCGGACGAAATCGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTCCCTGCCCC
GGGAGGTACTCTCGTGTGCGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTTGGGAGG
CTTTGCTGCGAATGTCTACGGGCTTCGAGCTGGGGAAGGACGCGCGCTCTTGTGTGACCA
GTGGGAAGGACAGCCGACCTTTGGGGGACCGGGTGCCACCAGGCGCCGCGCGGCACT
GCAACCAGCCCCGTGCCGACAGAAATGCGCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGCAATTTCAGTAACATCTATTCTGAGATTCTTCGATGGGGAT
CACAGAGACGATGTCTACCCCTCAAATGTCCCTTCAAGCGAGTCAAAGGCCACTATCACC
CCATCAGGAGCGTGATTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT
CGACTCCTCTGCGCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTACGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGGGCTGGAGAGTGATCTGAGCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGAAGTGATCTGCGGGACAGAG
CAGAGGGTGCTTGTGCGGGAGTCCCCCTTGGCTCTAGTGATGCAATAGGGAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC
TTGTGTAAGTGAACAATTTGTCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCCTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATAATTTCTATGTTTATTCGGAGAA
TTTGAGGAAGTGATTGAACTTTCAAGCATTGGAACAAATAGAACACAATAATAATTACA
TTAAAAATAAATTTCTACCAAAATGGAAGGAATGTTCTATGTTGTTCAAGCTAGGAGTAT
ATTGGTTCGAAATCCAGGGAATAAATAAATAAATAAAGGATTGTTGAT

0906348.071301

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACCATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI PVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCCTTTAAAAGTGCCCTCCGCCCTGCCGCGCCGCGTATC
CCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGCGGTGTGTGCCGCGCGCGCGCGCGTGGGGTGCAAACCCCGAGCGCTCTACGCTGCCATGA
GGGCGCGGAACCGCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTCACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCCTCCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCGCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAC
CTGTGCCCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG
CTTCGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGGATTACCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTCACT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTAGGCCAAAA
AAACTGCCTACAACATACAGAACAGCCTGTACCACCACATTCCCTGTAAACCAAGGTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAGAGGGAAATTTGGCGATTAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAAACAGTGAACCTGTGTCCATTTAAGCTGTATTCTGCCATTGSCCTTTGAAAGATCTATGTTC
TCTCAGTAGAAAAAAAATACTTTATAAAATTACATATTCTGAAAGAGGATTCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCCT
TGCTGCTGTGAGAGGAGCAGCTATCTGATTGGAACCTGCGGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT
GTTATTGTTTCAACCTTCAAGCCTTTGCCCTGAGGTGTTTACAATCTTGTCTTGCGTTTTCTA
AATCAATGCTTAATAAAATATTTTAAAGGAAAAA

09905448.071301

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERFVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVNLNFRFIDLESNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEFNERGDQYCGGLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSTADGFIGHYIFRPKKLPTTTEQPVTTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTATACCTG
CCGGGGACTGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAATACAAAGACAGTGAGACCCGCCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGSTATGTTCTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAAGTGTGTCATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTGAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTCGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTACAATGTGTGA
ATTTCAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG
GTCTCAGAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCTCTGT
TCTGTGTTACACATCCCCACACCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCCTTGAAAGTTAAAAA

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGTTCTT

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPPQSSPPPPQHPCHTCRGLVDSFNKG LER
TIRDNFGGGNTAWEENLSKYKDS ETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLC CPAGTFGPSCLPCPGGTERPCGGYGQCEGE GTRGGSGHCDQAG
YGGEACGQCGLG YFEARNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCDVIDE
CGTEGANC GADQFCVNT EGSYECRDCAKACL GCMGAGPGRCKKCS PGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG
IIICALATLAAKGDLVFTAFIGAVAAMTGYWLSERSDRVLEGF IKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

09505493.071501

FIGURE 41

TGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCCCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTACGCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACCTGCTGGTGTTTCGG
CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCGGGC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCTGCCACGAGAGCGGCTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAAGTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTGCAGCTGCCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGCGCCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAAGTCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAAATTTTGGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTATTATTCACCTGCACCTATATTCAAGCACTTACAT
GTGGAGATACTGTAACTGAGGGCAGAAAGCCANTGTGTATTGTTTACTTGTCTGTCTAC
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAAATGAATAAAACATTTTATTCT
AAAA

090548 07304

FIGURE 42

MQPLWLCWALWVLPASPGAALTGEQLLGSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLG DYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWWF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKSCASD GALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAAGGAGTCTTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGAATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCTCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTCT
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCCCTGTGAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTCTCGTGGCAGCCGTCCTTGTAACCCCTGATTCTCTGGGAAT
CTTGGTTTTTTGGCATCTGGTTTGCCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCCTGGTGTTGAGCCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCGTAGTTTTACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCTCCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGCCCTGGAACCTTGTTTTAAA
GTGTTTTATTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACCTTGAAAGCCAAAAG
GATTTAAAAACCGCTGCTCTAAAGAAAAAGAAACTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGATGCCTGTATGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

03905348.071301

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTRLVVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYYTCMVSEBGGNSYGEVKV
KLIVLVPPSKPTVNIPISSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRRGHFDRRTKKGTSSKKVIYSQPSARSEGEFPKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

105270.8422060

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGTTGGGACAGCAATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTCCGCGACCAAGTGGCTTATGCGTGCCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCGAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGAGACCAAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAGCCTGGTCAACGCCACCCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGCTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGACA
GGAGGAGAGCAGTGTATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACC CGAGCTCCTG CAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGCGAGCTCCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

0905348.071307

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDCSDGSDEEEECRIEPTQKGQCPCPPPGPLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGELRCTLSDDCIPLTWRC DGHPCPDSSDELGCCTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTS LP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTACGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGGT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCAATCCCGAGAATGGCTTCAGGACCCCGAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCAGTCCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCTTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGCATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGTGCGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCGTCT
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAACGTGTGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTGCTGCTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTATCCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCACAGGGGAGTCAGAAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGACCCACCCTGCTTCGGACAACCTTGACATA
ATTGCCAGCAGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCCACTGGGT
GTTGTTCTTAAGAAATGATTGATTAATAAATTTCCAAAGTGTCTGAAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTCTTGGTTTTAGACAAATGTAACAA
AGCTCTGATCCTTAAATTTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAGNAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKIITCQYGEWFPSPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

000034-071001
T02720-000000

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTGCGCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGCACGCGCTCTGCCCGCCAGCCCGCTCCACCGCGGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTCGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAAATTAGGAAC TGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGTGCAACATGAAGAACAAATTCATTTCGAAATATTCGTAGAGAAACGAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCTTGTGGTCACCACAGTGTGATGTTGGGTTT
GGATCTGTAGAAAAAGAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTTTCATTCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA
GTTCTCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAACTGACAACAAATGGAAAAGAAATGATAAGCAAAATC
CTCTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGTGAGCCCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGAAAAACCACTCTGTTTTCCTTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAAATCCAGAATCTTTTCAAAGCCCATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

0905348.071301

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSD GDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPFYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREALNLAYILIPSIPLLLLLLV
VTTVVCWVWVICRKRKREQDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTTGGGGGCGCCCGCTGAGCCCCGGCGCCCCGAGAAGACTTGT
GTTTGCTCCTCTGCAGCCTCAACCCGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGTTGTCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGCTGGGCGAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCTGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGCCATCATCAT
CCACACTGATGAAGCAGATTGAAAGTCTTGATATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGAGGCAGACTGCCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTATATAAAGCAGGATGTGTTGATT
TTAAAAATAAAGTGCCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTFVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHNLPSCPMLKRFRARMIEQRAVDTSLYILPKEDRESLQMAVGPPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFLPLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPDLMFLNAMS VYTLSPKEYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

09905148 071301

CTCTCTCTTAACATACTTGCAGCTAAAACATAAATTGCTGCTTGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACTGCTTGGTCTATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACACAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCAGCTGGTGGGGGCCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAAGGACGTGGCTGTGTGTGTGCCGGGAGCTGGGCTGTGGAGTGCACAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATATGATGAAGATGCTGGGGCATCGTGTGAGAAACCCAGAGAGCTCTTTCTCCCCA
GTCCACAGAGGGTGTACAGGCTGGCTGACGGGCCCTGGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG
TGTGCCCGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAAGCAACCTTCA
GGATTGCCCCTCTTGGGCTTGGGGGAGAAAGACACTGCAACCATGATGAGAGACAGCTGGGTGCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGTATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTCTGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTCTGCTCAGTGTAGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTTCTCAGGCCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTTCCAGCCCTCCATAAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TCTCTAGAGAAACGAATTTTAAGGATAAATTTCTGAATTGGTTATGGGGTTTCTGAAATG
GCTGATACAACTGAATTAGATATAAAATTCGGTAACTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGGLHRCGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESSFSPPVEGVRLADGPGHCKGRVEVKHQNQWYTVTCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSSCSGREATLQDCPSGPGWKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGPHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

20250710 07:30:00

[illegible]

ACTGCACTCGGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTAC CAGGAAGAGTCTGCCGAAG
GTGAAGGCCATG GACTTCATCACCTCCACAGCCATCTGCCCCGTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCATACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAAAGTGGG
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCCAGAGGCAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATAGGAGCTGGGGTTTAACTACT
AAAAACTGAGAAATTAACATCTCAAACAGTAAAAAATAAAGGCGCGGCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGCCCCAACTTGTTTATTGCAGCTTATAATGGTTA

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLGCRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLVSNITADGSRYGVMDDTT
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCCTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTCTCTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTGTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCTTAATTTTCGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAAC TGATTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTTGAAC TCTGTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTGTTCCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTGATTGCACCTTAAATTTTGT
ATAATTTGTGTTTCTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAATCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

CGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA

FIGURE 58

MKFLLDILLLLPELLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKS
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGPFHKTLDLALALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRIMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

03905246 073304
T02720 84E0000

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCCGGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCGTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGGCCCTTTCAGGACTGAACATGA
AGAGTTATGCCGGCTTCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
TTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCCTTATGTTGTGCACAAAGTAAACATGA
CCTTGGCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACTAATTGAGTTTTTCCAGATATTTCTGTAATATAAAAAATA
ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTTGGAGA
TGGATATTTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAAATTCCTGTACCAAAATTTGGCT
TGTTGGATGAGAAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGGAGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAAATGTTACAGGATGTAGTAATTAATAAATTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAAATGATGGAATATAGTTGAAAAGTACTTTGCGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAGGATCCAGGAATAACAAGAAGGCAGAAAAAAAGTTTGAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTACATGATTAAATCGA
TTCATTTTATGGAAGGATGGGATCCTTATGTTGGATAACTACCTTCCCAAAAGAGAACAT
CAGAGGTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAAATATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGATATAATGA
AATTTTAGGCTCTTGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAAAGTGCAAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTTATGGATAAGAAATAGCTCAATTATCCCAATAAATGGATGAAGCTATAA
TAGTTTTTGGGGAAGATTTCAAATGTATAAAGTCTTAGAACAAAAGAAATCTTTGAAATA
AAAATATTATATATAAAAGTAAAAAATAA

0905348.071301

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPVYVTSNMTLRDRDFPWTTLTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQT
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKQYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNVITG
CSNIYNFLRCTEPEDQLYVVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIIYNGQLDIIIVAAALTERSIMGMDWKGSGQYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

106770 8165060

FIGURE 61

CGAGGGCTTTCCGGCTCCGGAATGGCACATGTGGGAATCCAGTCTTGTGGCTACAACAT
TTTTCCCTTTCCTAACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCAGCTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCTGCCCTAACCAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTGTCTTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAATAAAAAATTTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCCTGGGTC
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTAATTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAAATCATGTGAGGGCCAACCGGGGAGGTGGAGCAGATGAGCACACACAGGAGCCGCTCT
CCTCACCGCCGCCCTCTCAGCATGGAAACAGAGGCGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTCAACCACTTGACCGT
CCACCAAGGAGCGGGGCCGTCTATGTGGGGCCATCAACCGGGCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCCGCTCTGCGCTGTGGGAGCCTTACCAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGCTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCTGTCCA
GCCGAAGCTGCCCCGAGACCCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGTCTAGTGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTCTTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACTGTGCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCTCTGCAGGCTGCTTACCTGGCCAGCCTGGGGACTCACTGGCCC
AGGCCCTCAATATCACCAGCCAGGACGATGTACTTTGCCATCTTCTCCAAAGGGCAGAAG
CAGTATCACACCCGCCGATGACTCTGCCCTGTGTGCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCTGTCTACAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAAGGACGCTCCAGTGCAAGAGCGCCTGTCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACAGCCCTGGGAGGCTCAACTCAGTGGAGGGCTGACCCCTGTACACCAAC
CAGCAGGAGCTTCACTGACCTCTGTGGCCTCTTACAGGCTACAGCGTGTTTGTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTCACTCTCTCAGCAAGAGTCCCTCTTGGAAGGTAGCTATGTGTGGAGATTAACTATAG
GCAACTTTATTTCTTGGGGACAAGGTTGAATGGGGAGGTAAAGAGGGGTTAATTTGTG
ACTTAGCTTCTAGTACTTCTCCAGCCATCAGTCAITGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAA

0905349-071300

FIGURE 62

MGTLGQASLFAAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQFPW
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFI LVEPSHKHEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFA SGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLF AIFSKGQKYHPPDD SALCAFFIRAINLQIKERLQSCYQGE GN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRC SNAIHLLSKESLLEGSYWWRFNRYQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGC GGACTGGAGTGGGAACCCGGGCTCCCGCGCTTAGAGAAACACGCGATGACCA
 CGTGGAGCCTCCGGCGGAGGCGCGCCGCGACGCTGGGACTCTCTGCTGCTGGTCTGCTTGGGCTTCTCGGTGCTCC
 GCAAGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
 ACTTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCGTGTGCCACGGGAGTACT
 GGAGGGACCGCTGCTGAGAGTGAAGGCTTGGCTTGAACACCTCACCACCTATGTTCCGTGGAACCTGCATG
 AGCCAGAAAGAGGCAAAATTGACTTCTTGGGAACCTGGACCTGGAGGCTTCGTCTGTATGGCCGACAGAGTAC
 GGTCTGGGGTGAATTCTGGCTCCAGGCCCTTACATCTGCAGTGAGATGGACCTCGGGGCTTGGCCAGCTGGCTCG
 TCCAGAACCTTGGCATGAGCTGAGGACAACTTACAAGGGCTTACCGAAGCAGTGGACCTTTATTTGACACC
 TGATGTCACGGGTGGTGCCATCTCCAGTACAAGCTGGGGGACCTATCATTTGCCGTGCAAGGTGAGAGATGAATATG
 GTTCTCTATAAAGACCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGGTGCCATTTGGAACCTGC
 TCTGACTTTCAGACAACAGATGSGCTGAGCAAGGGGATTTCTCCAGGAGCTTTGGCCACATCAACTTGCAGT
 CAACACACGAGCTGCAGCTACTGACCACTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGTGTATGGAGT
 ACTGGACGGGGTGGTTGACTCGTGGGGAGGCCCTCACAATATCTTGGATCTTCTGAGGTTTTGAAAAACGGTGT
 CTGCCATTGTGGACGCGCGCTCTCCATCAACCTCTACATGTTCCAGGGAGGCCAACCTTTGGCTTCATGAATG
 GAGCCATGCATCTCCATGACTACAAGTCAGATGTCACGAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
 ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
 ACCTTCTTCCCAAGATGCGGTATGAGCCCTTAACGCCAGTCTTGACTCTGTCTGTGGGACGCCCTCAAGTACC
 TGGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT
 TCGGGTACATTTCTATGAGACCGCATCACTCTGCTGGCATCTCAGTGGCCACGTGCAATGATCGGGGGCAGG
 TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCTCATGACAGGTT
 ACACCGTCTGAGGATCTTGTGGAGAACTCGTGGGCGAGTCAACTATGGGGAGAATATGATGACACGCGCAAAG
 GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACTTCAGAACTATAGCTGGATATGAAGAAGA
 GCTTCTTTCAGAGGTTTCGGCTGGACAAATGNGTTCCTCCAGAAACACCCACATTAACCTGCTTCTTCTTGG
 GTAGCTTGTCCATCAGCTCCAAGCTTGTGACACTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGATTTCA
 TCAATGGCCAGAACCTTGGACGTTACTTGAACATTTGACCCAGCAAGAAGCTTTTACCTCCAGGTCCTCTGGTTGA
 GCAGCGGAATCAACAGGTCTGTTTGGAGAGACGATGGCGGGCCCTGCAATACAGTTTCAGGAAACCCCCC
 ACCTGGGCAGGAACAGTACATTAAAGTGAAGCGGTGGCACCCCTCTGCTGTGTGCAAGTGGGAGACTGCCGCTC
 CTCCTTGAACCTTGAAGCCTGGTGGCTGTGCCCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACTCAGG
 ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTTAAGCCTGACGGGAAAGGTGGGATGGCTCTGGGC
 TGGCTTTGTGTATGATGCTTCTTACAGCCCTGCTCTTGTGCCGAGGCTGTGGGCTGTCTTAGGGTGGGAGC
 AGCTAATCAGATGCCCCAGCTTTGGCCCTCAGAAAAAGTGCTGAACGCTGCCCTTGACACCGAAGCTCAGAGCC
 TGCAGCATCTGTGGACTCAGGCGTGCTTTTGTGTGTTCTGGAGGCTTGGCCACATCCCTCATGGCCCAT
 TTTATCCCCGAATCTGGGTGTGTACCAAGTGTAGAGGTTGGGGAAGGGGTGTCTCAGCTGAGCTGACTTTGTT
 CTTCCTCAAACTTCTGAGCTTCTTTGGGATTTTGAAGGAACCTGGAGTGAAGAACATGTAGTCTCCCTT
 TCCCTTCCACTCGTGTCTTCCACAGGCTGACAGGCTGGGCTGGAGAAACAGAAATCTTCACTCCCTCGGTCTCC
 CAGTGTAGCAGCTCTGTGTGTTTCAAGTGGAGGAGACATGTGAGTCTTGGCAGAGGCAATGGCCATGTCTGCA
 CATTCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAGGCAATGGCCATGTCTGCAATCC
 AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAGGCAATGGCCATGTCTGCAATCCAGGGAG
 GAGAGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAGGCAATGGCCATGTCTGCAATCCAGGGAGGAG
 ACAGAAGGCCAGCTCAGTGGCCCTGCTCCCAACCCCAAGCCGACAGGGGACAGAGGCAAGCTCTTCT
 GAAGTGTGTCCAAGTCCGATTTGAGCCTTGTCTGGGGCCAGCCCAACCTGGCTTGGGCTCAGTGTCTGTA
 GTTGCAGTAAAGCTATACTTGAATACAA

0905348.071301

FIGURE 64

MTTWSLRRRPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLMKMACGLNTLTITYVPWNLHEPERGKFDGSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPWLLQDPGMRLRTTYKGFTEAVDLYFDHLSRVVPLQ
YKRGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLEFNVQGTQPKMVMEYWTGWFDWGGPHNILDSSSEVLKTVSAIVDAGS
SINLYMFHGGTNPFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSGISGIP
LPPFPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLIQGYTVLRLIVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPKFNRIYSLDMKKSFQRFGLDKWXSLPETPTLPAFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCCTTCGGTGGGGGTCAAGACGCGGACCTTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCTGCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTCTGTTCTAGTGGATAGGGGTCTGACCCGGTTCTCCTAGACGGGGGCC
CGTTCGGCTATGTCTGGCAGCCTGCACTACTTTCCGGTACC GCGGTGCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCGTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTGTGTCATACTGAGACCAAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTTGGCCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
CATGCTTTTATCACATATGGGGGCAACATCATTAGCATTCAGGTGGAGAAATGAATATGGTAGC
TACAGAGCTGTGACTTCAGCTACATGAGGCCTTGCTGGGCTCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTTCACCACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCCTGTAGATTTTGGCCAGCTGACAACATGACCAAAATCTTTACCCCTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGCTGTAACCAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTCAACACTTTGGATATTGG
AATGGTGGCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCACTAGCAAGT
TCCAGGAAGTTCCCTTTGGGACCTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATACCATTTTGAAGCAACACCATTCGGGTGCCAAATAATGGAGTC
CATGACCGTGCCCTATGTGATGGTGGATGGGGTGTCCAGGGTGTGTGGAGCGAAATATGAG
AGACAACTATTTTTGAACGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTCAGTGCCCAAGATTCTGTGTTTCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAATCAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCATC
CTCAATAGCAGTAGTACTTTGACAGGACACATATCAATTCCGTTTACGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
CTGTAATCCAGCACCTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA
CCAGCTTGGCCAAACATGGTGAAACCCGCTCTCCACTAAAAATAAGCAAAATAGCCGGGCGTG
ATGTTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGTTGTACCCTGCACTCCAGCTGGCTGACAGTGA
GACCTCATCTCAAAAAA

0905348.07.1001

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRHDFLLDGGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIFYFVFNWYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TLRLKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVFMHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVFN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNS SDFKGLLKP
PILGQTILTQMMFPLKIDNLVKWFPPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDFTFLYL
PGWTKGQVWINGFNLGRYWTQGGPQQTLYVPRFLFPFGALNKITLLEEDVPLQPQVQFLD
KPILNSTSTLHRTHINSL SADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTG
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTATGTGACATCCAGATGTCAAACCAATTTT
GCGTTCCTTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTGAGAAGTTAGTGAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCAGAGAAGCTAAATTCCTGCTAAGATTTCTCAATGACTAACCTCCAAGAGCTCCACC
TCGCCACTGCCCCTGCAAAGTTGAACAGACTGCTTTTAGCTTCTTCGCGATCACTTGAGA
TGCCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACCTCTGAAACCAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTTCTCCACGTGAAGAGCAATTTGACCAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAGTTAGTCATTACATAATGACGGCAC
TAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTCCAGCATTTAAACGACT
GACTTGTTTTAAATATGGCATAACAAAATGTTACTATTCTCCTCTATTACCCTATGTCA
AAAACCTGGAGTCACTTTATTCTCTAACAACAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGTCATATCACTGGGAACAAAGTGGACATTTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGACCGCCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTGTATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTTTGCAAATGGGATTTAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AATTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTAAAGTCATTCATTTCCAATCATTTTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATATAATCACTAATCTTGGTCTTTTTTAAATGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTCAAAATTGCTTGCCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAA

FIGURE 68

MAYMLKLLISYISIIICVYGFIPLYTLFWLFRIPPLKEYSFEEKVREESSFSDDIPDVKNDFAFLLHMVDQYDQLYSKRFGVFLSEVSENKLEISLNHEWTFEKLQRHISRNAQDKQELHFLMLSGVPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLSENKMKIGLESRLRLHLKILHVKSNTLTKVPSNITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCCELERIPHAIFSLSNLQELDLSNNIIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESPLVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQTQLLELKGNCCLDRLPAGLQGCRLKKSGLVVEDHLFDTLPLEVKEALNQDINIPFANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

Figure 1

CCACGGCTGCGGGCTCTCTCTGGACCTTGGCATCTTCATCTCTTTTACATGGCAAACTGACTTTTTTATTTCTCT
TTTTCATCTCTGGGCGAGCTGGGATCTAGGCGCCCTGGGAAGACATTTGTTTTCACACATAAGGAT
CTGTGTTTGGGGTTTCTTCTCTCCCTCCATGATCTGGCATCTGCTAGTGGTTGTGGGGAGGGAGACACGTGG
CGTCACTGCTTGTCTGTCTATTAATCTGCTAGATGATCAAGATCTTTGAACTCCATACAGTGAATATGCTGT
ATGCTGTGGTGTATCTCGCGGGCTGCTCTCTCTGATAGTTGTCTGTCTGTCTTTACTTCAAAATACACAA
CGCTTAAAGCTGCTCAAAAGGAACTGAACTGCTGGCTGTAAAAAATACAAACACAGAGGCTGTGGTGGGCGAAG
AAGCAGCCAGGCCAAACCAATTGCCACGGAGTCTTGTCTGCCCTGCGAGTGTGTGAAGGATAGAATGTGTGC
AGTTTGAATCTGCTGCCAATCTGTGCTTGTGGCATATAATGAGGGCTCTGAGTGTAGAAGAGCTCCCTCTCTCAA
GCAGAGCCTTGAAGACTTCAATGATGTCAATGAGGCCACTGTTTGTGTGTGTGCGAGCAAGAAAGGACAG
CTCCCTCACTGATTTCTATGAAAATAACTCAGTGCCTGTCTGGAAACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGCAACCTCTCGAAGGAAGTTGGGAGAGAGAACCTCACTGTGGGAATGTGTGAATAAACAGTCA
CAAGCTGCTCTATTTCACAACTATACCCCTTGTGCTGGTGGGAGAACTGAGCTTTCCCTGGAAGTGTCTGAA
GCTGATGTAAACAGAGGCTATAAAAGCTGTGGCTCTTAAAGCTGCCAGCGCTTGCCTGAAATGGAGCTGTGA
AGAGAGCTCATGCCATGTACCTCTTAATTTCTCTCTGTGTGGCGGAGCTGACAAATGGCGGAGGCTGAGGCAAT
CGAAGCTGCAACAGTCAGTGTGGGGGTGCCAATGTGGCAGAGACCAAAAGCCATGATCTGCAACTCAATCCC
AGTGAAGACTCCACCTGGCAATAGAAAGACCAAAACAAAGCAATTCAGAATATCTTTTCTATGTCCAGTGT
GATCCAGATGGAAGCTGTGAAAGTGAATAAATGAGCTTTTGAACGAACTCCAGCAATGGGCTCTGTGATGG
CAAGTCTGCAAGTAAAAACGACTATGTTCTGTGTTTAATCATCTCAAGTACATGACGTTTCAAAATGAGTTACT
GACTCAGCAAGAAATCAAGAAGACTGTCTTTGTCTCTACTCTTCTTCTCTCTAACTCTATTATCCAAACTGT
GGCGGTTACTGCGATATCTTGAAGAGATCTCTCACAGCCGCAATTAACCAAGACCGCATCTCTGAGTGGCTT
TGTGTGGGCATCAACAGTGGGAAGAATACAGAATAAACTAAACTTCAAGAGATTTCCTAGAAATAGAC
AAACAGTGCCTGCAATTTGATTTTCTCTCTCATTAATGTGCGCCCTCCACAACTTGTGCTGCAATGGACAGCTGT
GGCCCTGTGACTCCCACTCTGAATCTGCATCAAGTCTCTGTACTGTGTGTGTGTACAGATTTAGCAATCT
TACCGGGGATTTCTGCTCTCTCACTCACTCAATTAATGTGCAAGAAATCAACATCAATCTTAACTGTCTCT
TACAGGCTGAGAGTTATTAAGCAAACTCTACTGAGGCTTTTAACTCTAAAGGGAATACTGCAACTAAAA
GACCCAACTTGCAGACCAAAATTTCAATGTTGTGGAAATTTCTGCTGCTCTTAATGGATGTGTGCAATCAAGA
AAGTGTAGAGATCAGTCAATTACTTACCAAAATAATTAACCTTTTGTGCTACTCAACTTCTGAAGTGTACCC
CGCTGAGAAATCACTCCAGATTTCTGTGAAGTGGAAATGGGACATAATCTACAGCTGGAGATATATACATCA
GAGTATAGTATTAACAAAGTCAAAATGACTGGGCAATAACACAGCAATGCTCTTTTGAATCAATTA
TTTGAAGAAGACTATCTGAATCACCATATTTGTGGAATTTGAACCAAACCTTTTGTTCAGTTGATCTGTGAC
ACCTCAGTCAAAATTTGGTGGTGTTCCTGATATCTGAGACTCTCCCACTCTGACTTTGTCTCTCAACC
TAGACCTTAATCAAGAGTGGATGTATGCTAGATGAACTTGAAGGTGTATCCCTTATTTGGACACTTGGGGA
TCTCAGTTTAATGCTTTAAATTTCTGAGAAGTATGAGCTCTGTGATCTGCAGTGAAGTTTGTATGTGTAT
AGCAGTGACCAACGAGTCTGCTGCAATCAAGTTTGTGTCTCGAAGCAAAAGACGACATTTCTTCATATAATGG
AAAAACAGATTCATCTATAGGACCAATCTCTCTGAAAAGGATGAAGTGAAGTGGCAATTCAGGATTCAGCAT
GAATACATCTGGGAGAAATCTCAAAACAGCTTTTCAACAGTGTGATCTGTTTTCCTATGTTTCTAGCTCTGT
GATGTGGTGAATCTGACGCAACATCAAGTGAAGCATTTTGTAAATCAAGCGGACATCAAAATCAGGAGCTGT
CAGAATCATTAATCAACAGGCTCAACCTTAAGTGAAGACATGTTCTCAGGATGCTCAAGGAGGCTACTCTGT
GGTACATCATATTTATGATAAATAGGAAGGGCTCGAAGTGAACACACAGGCTGTGATGTAAAAAA

FIGURE 70

MELVRRLLMPLTLLILSCLAEITMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIIRIIFSYVQLDPDGSCSEENIKVFDGTSSNGPLLQGVCSKNDYVPVFESSSSLT
FOIVTDSARIQRTVFVFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVVHHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSSNLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPIYYVDLNTQLFPVQVSLHTSDPN
LVVFLDTCRASPTSDFASTPYDLIKSGCSRDETCVYPLFGHYGRFQFNAPKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSTIIGPIRLKRDRSASGNSGPFQHETHA
BETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTG
TGCTGCCGCCGCGCCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC
CTGGACGCCGCCGAGCTGCCGCGTGTTGACCAAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT
TTTGAGACCATTATTACAGCAAAATTTTTAATGCCAACAGTGGGCAGATATTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTTCGTGGAATCGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACGAACTGACCTGCGTTTTGGACTGTACTATTCCCTTTTTGA
ATGGTTTCATCCGCTCTTCTTGAGGATGAATCCAGTTCATTCATAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACACTATCAGCCTGAGGTTCTGTGG
TCGATGTTGACGGAGGAGCACCAGGATCAATACTGGAACAGCACAGGCTTCTTGCCCTGGTT
ATATAATGAAAGCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAACTGCATGACAATAGACAACTGTCTCGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCACACTAGATGGCACCATTCTCTGAGTTTTTGAG
GAGGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCGCATTTTTCTTAATGGCCACACTCAGGACAGCTGTTCTCTGGCCAT
CCCAAGCTATTCTGGGGCAAAGAGGTGAAACTACTGGGCATGGACAGCCACTTAACATG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCATGGAGA
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTCCACTA
AATTTTTCTTAATTAACCATGTAACTATTTAACTCTCCAGTGACATTTGCCATTAAAGTC
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAAATTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATTTTTCTGGGAAATGCATTCTAGTCAAT
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATAGCTGAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAATACTGTAAATAAATGTTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACTGCCAGAGCTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAA
GTTTTCTTTCTTCAATTATAAATAAATAAGTGTACTGTAACTTTACAAACGTTTTAATT
TTTAAACCTTTTTGGCTCTTTTGTAAATAACACTTAGCTTAAACATAAACTCATTGTGCAA
ATGTAA

0906548.071301

FIGURE 74

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAPFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT DKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGCTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGTGTCCTTCTACTCTGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCCGCTTGGATATTCGCATGGGCCCTACTTTACATCACACTCTGCATAGTGTTC
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGTATACTGATGTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAATATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCAGTGTGAGA
TGGGGAACAAGAAGGATAAA TAAGATCCTCACTTTGGCAGTGCTTCTCTCTCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG
CTGNGACTGGNTGGGCGAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTGAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAATGTTTCCCTCCAAGCTTGGGTCACTGTGTTAACTGCTTATC
AGCTATTACAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTTCCCCAAGGACTCTTGCTTCCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAGATATAAGCCTAACTTTGTGCTAGTCTTAAGGAGAAACCTTTAACCAAAAG
TTTTTATCATTTGAAGACAATATTGAACAACCCCTATTTTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTTGACTTTTAC
TAACCCCTGACATACTCCCCACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIAIVYSVPRLSRWLAQPPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

16605348-071301

FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGGCCCTG
GGGCCCCAGCCTGGCCCCGGTCAACCCTGGCATGAGGAGATGGGCCCTGTGTCTCCTGGTCCCA
TTGTCTCTGTCTGCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCTGTTCACTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGGCGTGTGCGTGTCAAATGGTGAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGTGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA
GGATGAAAGCGGTCTGTGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA
ACGGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCC
CAGGCCCTGGCACCTGGCGTGCGAAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC
AGCTCTTTGCGCCTGGAAGTTCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGTACCTGTGGTTACCCGCATCCTAAGTGTGGGCCCCAGAGCCTGGGGT
CCGAAGCTTTGGCTTCCCGACCCGCAGAGCCGCTTGTAAGGTGTTTACTGTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCTGCCGATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT
CGTTTTCCCTTGTGGGTTGGAGCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTTACTATTTTTGTAAAGCAAACAGAACC CAATGCCTCCCTTTGCTCTG
GATGCCCCACTCCAGGAATCATGCTTGTCCCTTGGGCCATTGCGGTTTTGTGGGCTTCTG
GAGGGTTCGCCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCT
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCTCCCGGTTCCCTT
TCCCTCTCGGTTCCAAAGAATCTGTTTTGTGTGTCATTTGTTTCTCCTGTTTCCCTGTGTGG
GGAGGGGCCCTCAGTGTGTGTACTTTTGACAATAAATGGTGTCTATGACTGCCTTCCGCCAA
AA
AA

090548.071301

FIGURE 78

MGLLLLVPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRR LHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTC TGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACAGGGAA
CTTCAGTACGACCATGAGGCTTTCTGGGACGGGAAGTGCCAAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGCGCCACTACGCGCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGCGTTCCTCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG
AGTTCCTCACATGCGGGACATCGTGATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCGGGACTTCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCACTGGGTGCTGCCCCCTGCCCAGGACCAAGCCC
CTGGTGGAAGCCAACCACTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCAAGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCTGCCCCTGGGCTCTCAGGGACCCCTGGGTGCGCTTC
TGTCCTGTGCACCCCCAACCCAGGGAGGGGCTGTCTAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTCAGTCTTAA
GAACGCCCCAACCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCTT
GGCCCCAGCCTCTCCTGCCCTGGCCTGGGACACCTCCTCTCTGCGCAGGAGGCAATAA
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

000546.0730

FIGURE 80

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGVWEEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDGSMATRE
BLTAFLHPPEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCCTTCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCGTCCCAG
CCTGTCTGTGTCGTTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTGTCACACCGATCCTG
GGCTTCGCTCGATTGTCGCGCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCCTGGAGCAG
CGGGTCGTCTGTGTCCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCGCGGGGCTCCCGCACCCTGGCCTTGCCCGCATTCTCCCTCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCGCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG
TGTCGTGCTGCTGCTGCCGGGGCCCCGGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCAGATG
TTTTACCAGAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGAAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCCTACC
TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTTAGAT
GGTCTGCTTCTTTCACAGTAACATAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAACGACTAAAGAAAAACCCGAGAAGAAAACTGG
CAATAAAGATTGTAAAGCAGACATTGCATTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTACAGAAGAATTTTGTGGAAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCCATGTGGGCCTTGTTCAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA
AACTTTACATCAGCCAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCCAATCAGGAAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGATTTTATGTATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCAATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCCAAAAATACGTAAA
GCCTCTGTGACAGAAGCTGTGCACCTCATGAACAAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCCTTTCTAATTTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACGTGACTATAGCACCA
AAGAGAATGTCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
GATGCCATTTCTTCTCACTGTTAGAAATGTGTTTGGCCCTATAAAGGGAGAGCCCCAACAGAA
CTTCTAGTAAATTGTACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCAGTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGTTTACAGGATT
AGAACCAATTGTTTCTGATGTCATCAGAGGCATTGTAGAGATTTCTTAGAATCCCAGCAAT
AATGGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGTATGTCAAC
AGCCATTTAGGCCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCAATATCATGGCTCTTAGAAACTCAGGAAGAGAGGA
GATAATTGGATTAAAACTTAAAGATTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAGAATCTGATACTTAGACCAAAAAA

09065348.071301

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPAIATCTRGLDIRKEKADVLCPPGCGPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSSTQEATGQAVSTAHPPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFGRGNSNTGKAL
KHTAQKFFTVDAGVRKGI PKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVT FVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLC THEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCGCGCTCCCGCACCCGCGGCCGCCACCGCGCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCCGCGGGGAGCGAGCAGATCCAGTCCGCGCCCGCAGCGCAACTCGGTCCAGTCG
GGCGCGGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCGCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCCGCGCGGCTCTCAGCTACCCGACGAGGAGGGCCACCCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGTGTGAGGAGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACTTACCTCCAGCTAT
CACAATGAGACCAACACAGACGAAAGTTGGAAATAATACCATCATGTGCACCGAGAAAT
TCACAAGATAACCAACACAGACTGGACAAATGGTCTTTTCAGAGACAGTATCATCATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGTCATCATCGACGAGGACTGTGGGCCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAAACGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCTTCCAGAGAGGCGCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTTGGACCGATGCGCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTCGAAGCCGACCTTCTGTGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGTGGGGGAGCCTGCGGCTGCCCGCGCT
GCCTGCTGGGAGGGGAAGAGATTAGATCTGGACAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA
TCTTCTTCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTACG
TCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTCTGGGAGGATCAGGCGAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCTCTACAGTTTGGCAG
ACAGCCGTTTGTCTCATAGGCTTTGATAATTGTTTGGGGAGGAGATGGAACCAATGTGG
AGTCTCCTCTGATTGGTTTTTGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAACATCAA
CCTGGCAAAATGCAACAAATGAATTTTCCACGCAGTCTTTCATGGGCATAGGTAAGCTG
TGCCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCGTCAATACATGTGTTTATTCAATC
AGCAGTGTGTCTCAGCTCTTCACTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCTGGGGAGGGGTCATTGTTCTCCTCGTCCATCAGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCAACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGTTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACACAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAAATGGGATTTTCTTGAGGATGCACATCTGGAATTAAG
GTCAAACTAATTCTCATCTCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGCTCTAATGAAGACAAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCTATTAGTAACCTTGAAGGTATATGACTGAGCGTAGCATACAGGTTAAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAAATTATCAACACGTGGAGAAATCAAAACGAGCAGGCTGTGTGAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCTCCAGAGTCTTAAAGTTTAAAGTTGCACATGATTTGA
TAAGCATGCTTTCTTGATTGTTTAAATTTATGTATAAACAATAGTTGATTTAGAAATCAAGC
ATAATCACTTCACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

0900546.071301

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEAAAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQRMMLCTRDSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGGCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEET

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

05455-07301

AAGAGGCTCTGGGAGGAAAAGGTTAAGAAGGTTTGAAGAAGCTACCTCACAATCTCTCTGGGCTCAGAGGAGCTCTG
AAGATACACATAATTCAGCCGCTACCTACTCTCTCCCTCCCAACACACATGTCAGTATGACACACATACAC
CACACATACACTCTCTCTCTCTCTCTGACAGACTCAGTCACTCACTCTGTGTGACGAGCTCTATAGAAAAGGACAC
TAAAGCTTTAAGGACAGGCTTGCCCATCTGACCTCTGCAAGCTCTTTGGGCTTTGGAGTCAAAAAAGCTTGGAGGGG
CCAGGCACGCTGACTCACAACCTGTTATCCAGCAATTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTGGAGG
TTCGAGACCTGCTGCGCCCAATCTGAGCAAAACCCCATCTCTACTAAAAATAAAAAATGAGCCAGAGGTGTGTGCT
AGGTGCTCTGTAATCCCGACTACTCAGGTGGCTGAGCGAGAGAATGCTTGTAATCCAGGAGCGGAGGATGTGAGC
CGCTGAGTGACACCGTGCATCTCCAGCCTGGGTGACAGAATGAGATCTGTCTCTCAAAACAAACAAACACGGGAGGA
GAGGTAGATGACTGCTCTCTGCAACTCTTTTAACCTGTCACTCTCTTTCCAGGAGCTGCCCTCAGTGGGGCTCT
GCATGACTGTAGGACGGCCGACCCGAGGAGACAGGAAGAGGAGCAATTTAGGAGGCGGAGAAAGTGACGCCGT
GTGTGAATGACTGCCCTGGGAGGCTGGTCTCTGTGGGCGGACGAGGGTTCTGACCTTACCTCGAAAAACAACA
AAGAGCAGGAGCTCAGACTCTCTTTGTGAATGTCCCTCTGCGCTGCAAGCTCACACTGAGGCTTCTGTGTGGCCCC
ACTCTTCTGAGCTTGGGTGGTGTGGTGCACTGCCATGCCATGTGCGCGTGAGTACCTGCAATGTTCCTCGGCCCTCA
GTGTGCTGCGACGATCTCGCGCCTGTGTATAGCGCCCGCTCTCTCTACCGGAGGCTACATCTGTGTGACTGCAATGAC
CTATTTCTGACGCGAGTCCCCCGGCATCTCCGACGAGCACAGACCTGCTCTGAGAGACACAGCATTTGT
CCGTGTGAGACAGAGTAGTGCTGGGCTACTCTGGCCAATCTACAGAGCTGGACCTGTCCCAAGACAGCTTTCTCGGA
TCCCGGAGCTCTGATTTTCATGCTGCTCCCGACTGTGTAGCTGTCACTAGAGGAGAACAGCTGACCCGCTCT
GGAGACACAGCTTTCTGAGGGCTGGCCAGCCTACAGGAATCTTATCTCAACCAACAGCTCTTACGATCTGCG
CCCGAGGGCTTTTCTGGCTCAGCAACTGTGTGGGCTGCACTCAACTCAACCTCTTGAGGGCTATGTAGAC
GAGCTGGTTTGAATGTCTGCCAACTGTGGAGATCTCATGATGTGGCGGACAAAGGTAGATGCCATCTGTGACAT
GCACTTCTCGGCCCTGTGCACAACCTGTGTGCTGGTGTGACGAGGATGAACCTGTGGAGAGATCTCGCATGTG
CTGTGAGAGGGCTGCAAAAGCTGGAGAGCTCTCTCTTATGACAAACCTGAGCTGGCCGGGTGTGGCCGCGGAGCT
GGACAGGCTGCTCGGCGCTCAAGTCTCTAGACTCTCAACAAACCCCTCAGCGGGTATGCCCAGCGGGAGCTTGC
CAACTCTGTCACTTAAAGACTTGGAGCTTAAACAACATGAGGAGCTGTGCTCTCATCGACAAGTTTGGCCTGTG
GAGCTTCCCAGAGCTGACAAGCTGTGACATCAAAATAAACCCAGGCTGTCTCTCATCCACCCCGCGCTTCA
CCACTCTGCCCCAGATGAGACCTCATGCTCAACACAAGCCTCTCAGTGTCTTGCAACGAGACAGGCTGTGAGTGT
CTCTGCCACCTCTCAGAGAGGTAGTCTCTCCAGCGCAACCCCATCCGCTGTGACTGTGTGATCTCTGCTGTGGCCAAATGC
CACGGGCTCCGCTGTCTGCTCTTACGCGCGCAATCCACTCTGTGTGGAGAGCTCTCGGAGCTCTCAGCGCTCTCC
GGCCCTGAGTGTGCCCTTCCGGAGATGACGGACACTGTTTGGCCCTCATCTCCCCACAAGGCTTCCCCCAAG
GCTCAGGTAGCAGTGTGAGAGAGCAGTGTGTGCTGCTCGGCGACTGGCGAAGCCGAACCGAGATCTTACTGT
GGTCACTGAGCTGGGCTCTGACTGTCTGACTGAGCTGCACTGCCATCGCAGGAGAGATCCGGGTGTACCCGAGGGGACCT
GGAGCTCTGGAGGTGACAGCAAGAGAGGACGGCTGTATACACTGTGTGGCCCAAGTCTGTGTGGGGCTGACAT
TGAGACGGTGTAGTGTGTGTGGGCGTGCTGCTCTCTCCAGCAGGACAGGGAAGAGGACAGGGGCTGAGCTCGC
GTGTGAGGAGAACCCACCTGTTATCATACCTCTGTATCTTGGGTCAACCCCAACACAGTGTGCCAACATCCAG
CTGTGTCAGTGTCTCTCTCTCCGGGGCAGGGGGCCAGAGCTGTGGCCGGCTCTCTCTGGGGAACCCACAGTAT
CACATATACCGCTCTCTCTCAGGCGACGGATGTGGGCTGCTGCTCAAGTGGGCTTTGTGTATGTCCCAACCA
GTGCTGTGTGTATGGCGCAGGACAAAGAGGCGCACTTCTTGCCACAGAGCTTGTGGGAGTGTGCTGTGGGCTCAT
TGTGCATCTGTGCTCTCGTGTCTCTCTCTGTGCGAGCTGGGCTGAGCGGCCACTTGTGACAGGCCAACCCAGGAA
GGGTGTGGGCTGGGAGGGCGCTCTCCCTCAGGCTGGGCTTCTTGGGCGTGAGTGTGCCCTCTGTCTCGGGTGTG
GTGCTGTCCCTGTGCTGCTCTGCAATCTCAGGAGGAGGACTGCCAGATCTCAGAGGGGAGGACATGTGTGGC
ACATGTTCTCAAAATTTCTGAGAGCTCAGGCTGTGTTCAGCAGTATGAGCAATCATCAGGACTCTTTTCAAAA
AAGAGAAGCAGTCTGGGCGAGTGCCCTGACAGGAAGGACATGACCAAGTGTCTTGTAGGCTCTGAGCTGTGGC
CAGTACAGATGGGGCTTTGTGGCCTTGGGCGCTTCTGTGAGCTGTGAAAAGTTGGCCCTTACTCTCTTAGGGTCA
CTCTGCTGTGCATCTGAGGAATCTCTCCAGGACAGGAGGGAATTTGGTGTAGAGCTCTGTGCTCCCTCATCT
CTCTTCTGCCACAGGCTCTGTGGCTGTGCTGTGCTGTGTGCTCTGGGACAGGCTGAGGAGGCCATCCATCTCAT
CTGGGCGGGCTGCCCTCAATGTGGGAGTGACCCAGCAGATCTGAGGACATTTGGGAGAGGGATGCCCGAGGA
CGCTCTCAGCAGAGCTTGGGCTGCATCTCCGAGCTGACTTTTATAGGCAATTTGTACCTTTGTGTGGAGA
ATGTGTCACTTCCCCAACCCGATCACTCTTTTCTCTGTGTTTGTAAAAAATAAAAAATAATAACATAAA
AATA

FIGURE 86

MRLLVAPLLLA WAGATATVPVVPWHVPCPPQACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLQLQNSIVRVQDQSELGYLANLTEDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLOELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWE
MLPNLEILMIGGNKVDAILD MNFRPLANLRSLVLAGMNLREISDYALEGLQSLLESLSFYDNQ
LARVPERRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKFKALVNLPL
ELTKLDITNNPRLSFIHPRAFHHLPQMETMLN NNALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPSPSLQ
VASGESMVLHCRALAEPEPEIYVWTPAGRLRTPAHAGRRYRVYPEGTLELRRTVABEAGLYT
CVAQNLVGADTKTVSVVVG RALLQPRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGGRRLPPAWAFWGSAPSVRV
SAPLVLPWNPGKRLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTAACCGCCT
 CTACATGCGGCGAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATGTGCTACACCGTCTACTACGTGCACAA
 CATCAAGTTGAGCTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACTACGCTGCTGCCACCC
 CCGTGGCCACACTCTTCAAGATCTCTGGCGTCTTCTACATCAGCCTAGTCTATCTTCTACGGGCTCATCTGCATGTA
 CACACTGTGGTGATCTACCGGCTCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
 CGACATCCCCGAGCTCAAGAACGACTTCGCCTTCATGCTGCACCTCAITGACCAATACGACCCGCTCTACTCTCAA
 GCGCTTCGCGCTCTTCTCTGTGGAGGTGAGTGAGAACAAAGCTGCGGCAAGCTGAACTCAACAACGAGTGGACGCT
 GGCACAGCTCTCGGCGAGGCTCAACAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCTATGCTCTAGTGGCAT
 CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCGCAGCTGACCATCCCGCC
 CAGCATTTGCCAGCTCAACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCGAAGATTGAAGCGCTCTGCGCT
 GGCCCTTCGCGGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGAGATCCCGCTGTGGATCTA
 TAGCCTGAAGACACTGGAGGAGCTGCACCTGCACGGGCAACTCTGAGCGCGAGAACCAACCGCTACATCTGTCTATCGA
 CGGCTGCGGGAGCTCAAAACGCTCAAGGTGCTGCGGCTCAAGGACCACTAAGCAAGCTGCCACAGGTGGTTCAC
 AGATGTGGCGCTGCACCTGCAGAGCTGTCCATCAACAATGAGGGCACCAAGCTCATGTCTCTCAACAGCTCTCAA
 GAGATGCGGAAGCTGATCTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
 CTTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCGGCAAGCTGCG
 CTACTTGGACCTCAGCCACAACAACCTGACCTTCTCCCTGCGGACATCGGCCTCTGCAGAACCTTCCAGAACT
 AGCCATCAGCGCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCAGGAAGCTGCGGGCCCTGCACT
 GGGCAACAAGTGCTGCACTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACTGACCGCAGTCGAGCTTGGCGG
 CAACCGGCTGGAGTCTGCTGCTTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
 GGACCTGTTCACAACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGGCTGAGCGAG
 GCGCGCCAGCAGCAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGCGAGGCTAGCTTCTCCAG
 AACTCCCGGACAGCCAGGACAGCTCGCGGCTGGGCGAGGAGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
 GGACAGTATCTGTGGGGCTGGCCCTTTTCTCCCTCTGAGACTCAGTCCCCAGGGCAAGTGCTTGTGGAGGAG
 AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCTCCCTGGAGGCCAGCTTGCCTCCAGGGGCTGAG
 CTGCCACAGAGGTCTGGGACCTCACTTTAGTTCTTGGTATTATTTTTTCTCCATCTCCCACCTCTTATATCC
 AGATAACTTATACATTCCCAAGAAAGTTAGGCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCTTTTCCCC
 TTGTCTTATTATAGCATGCGCGCGGCATTAAACACCCACCTGGACTTCAGCAGAGTGGTCCGCGGCGAACAG
 CCATGGGCGGTCAACCAGCAGTCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCTCCAGCTGGA
 AAGGCCAGGCTGGAGCTTGCTCTTCAGTTTTGTGGCAGTTTGTAGTTTGTGTTTTTTTTTTTTTTTAACTCAA
 AAACAATTTTTTTAAAAAAAGCTTTGAAATGGATGGTTTGGGTATTAAGGAAAAAATACTTAAAAAA
 AAAAGACACTAACCGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAGCAGCCAGACCT
 TGAACCTGTGTTCTCTTCCCTGGGCGCAGGGTGCAGGGTGTCTCCGATCTGGTGACCTTGGTCCAGAGT
 CTATTGTGTTCTGGGAGGAGGTTTTTTTGTGTTTTTGGGTTTTTTTGGTTTTTTTGTGTTTTCTTCTCTCC
 ATGTGTTCTGGCAGGCACCTATTCTGTGGCTGTGCGGCAGAGGGAAGTTCTGAGAGCTGCAGAGGAGGAGGAG
 ACTCGGCTTGGCTTAATCCCGGATGAACGGTGCTCATTCGACACTCCCTCTGCTGCTGCCCTGCTCTCCA
 CGCACAGTGTTAAGGAGCCAGAGGAGCAGTTCGCCACAGACTTTGTTTCCCACTCTCTGCGGATGGGTGT
 CCAAGTCCACCGCTGGCTCTCGCTGCTTCCATTCACCTCAGCCTGTGCGCACTGGTCTTCTGAGAGCAGACACTTA
 GGGCTGTGTCGGAATGGGAGGTGCGCCCTGGAGGGCAGCGGTGGTTCCAAGCCGGTTCCCGCTCTCTGGGCG
 CTAGGCTGCACACAGCCAGCTGCGGACCTGGTGGCTGAGAGCAACCTGTTAGACTCACTCGGGTCCCCACTT
 AGAAGGGTCTCCCGCTTAGATCAATCAGCTGGAACACTAAGSCACGTTTAGAGTCTCTGTCTTAATGATTATGT
 CTAACCGTCTGCGTCCATTTGTGTTTTCTGCGTCTGTGCTATTGATATATCTCAGAAAAATGACACTAG
 CCTCTGACAACCATGAAGCAAAAACTCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGATCAATAAAA
 ATCTATACAGAAAAAATAAAAAA

090548.071301

FIGURE 88

MRQTIKVIKFIILICYTVVYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHFLMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLLELHLTGNSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEBIDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

0005248.074301

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCCGCGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGAGAGCTGTCAATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACACGGAACCACTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCCATGAGGAGAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTGAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTGGATCTCCCCGTGTGATTGCGGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTGCGAGAGCAAGTA
CTGAATGCCGTAATAAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACTAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTGACGCG
CACGTGAGACACCTACAACGAGATGCCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTCGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGATAATGGACAGCTGGATCTCATCGTAGATACCATTGGGTGAGGAGGCTG
GGTGGCGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCTAAATCTTTGGAACATCTGCTTTTGTCAAGTCTTACAAGAACCCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGACAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAATTTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTA

0905348.07301

0905745-01301

Signal sequence:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCGCTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAATCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCAGGTCGCCATCATAACA
ACTCTATGTGAACCACCTCTTCTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
TTTGTGCTGGCAACGCCCAAGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTGTTGGTAATAAACACATTCAGTTGA
TGCTTGCAGGGCATCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRLW
DSHVCVGSLLSHRWALTAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSN
YLSPRYLGNSPYDIALVKLSAPVYTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKIDIFGDMVCAGNAQGGKDACFGDGGGLACNKG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCCAGCGTCCGCGGACGCGTGGGAAGGGCAGAA**TGGG**ACTCCAAGCCTGCCTCCTAGGGCT
CTTTGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCCGACCAGCGGAGGACGC
TGGCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
GCCTTGAGACAGCAGAAATGTGAAAGACTCTCGGAGCTGGTGAGGCTGTGTCCGATCCAG
CTCTCCTCAATACGGAATACTGTAGCCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCCACACGGTGCAAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTTCTEACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTTCATCATATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCCAC
ATCCCTACAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCAACCGT
TTTCCCCCAACATCATCCTTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATAACAATTGACCTCACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTTGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTTCATGCGCCTCTTGGTGCAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGGTGGACAACAGGGCCGGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCTGTCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAAGTTCGCCCTACCTTCCCTGCCTCCAG
CCCCATGTACACCAAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTCCACCGGCCCTTATACACAGGAG
GAAGCTGTAACGAAGTTCCTGAGCTCTAGCCCCACCTGCCACCTCCAGTTACTTCAATTGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTTCCATGGGTGTCCGGAACCTCGGCCCTCTACTCCAGTGTTTGGGGGGATCCTA
TCCTTGATCAATGAGCAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCGAGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTCTGTC
TGATGAAGAGGTAGAGGGCCAGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCCAGCTTTGCT**TGA**AGACTCTACTCAACCCCTGACCCCTTCCCTATC
AGGAGAGATGGCTTGTCCCTGCCCCTGAAGCTGGCAGTTTCAGTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGCAACCTCAACTATTGACTGTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTTAGATTCTCAATAAGATGCTGTAACCTAGCATTTTTGAAATGCCCTCTCCCTCCGC
ATCTCATCTTTCTCTTTCAATCAGGCTTTTCCAAAGGGTGTATACAGACTCTGTGCACTA
TTTCACCTGATATTCATTTCCCAATTCACTGCAAGGAGACCTCTACTGTACCCGTTTACTCT
TTCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACCTCTCAATCTTTGCTTTATG
GCCTTTCCATCATAGTTGCCACTCCCTCTCCTTACTTAGCTCCAGGTCTTAACTTCTCTG
ACTACTCTGTCTCTCTCTCTCATCAATTTCTGCTCTTTCATGGAATGCTGACCTTCATGG
TCCATTGTAGATTTTGTCTTCTCTCAGTTTACTCATGTTCTCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
TGTAATAAA

0905348.071301

00505346 07307

Signal sequence:

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

CCCCGCGCGCTCTCTCCCGCGGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGCTGCTCGGCGCGGAACAGTGCTCGGCATGGGCAGGGGATTCCAGGGCTCCTCTTCTCTCTC
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGTGCTCTTGCCCCAGTCTACCCCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCTATAAGGGAAC
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTCAGCATTTTTGGGAAGGACTTCTGTCTCACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAAGCATGTCTCAGAGCTGCCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCTTAAAGCCC
AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA
ATTTTCAGTGGATCCGGGTGAAACGCACCCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGTCTAAGCAGCTGCCAGGGGCGAGAATTCACCTTCTC
TGGTTATGACAATGACCGACCGAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCCAGCGAGGGGCCAGCGGCTCTGGGGTCTAT
GTGAGGATGTGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTTCAGG
GCACCAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG
TGAACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC
AAATGTITTTTTGTCTATTGGCGTGACACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACTG
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAAATAA
AAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACCTTTGATTTTTATTTCATCTGAACTTGTTTCAAAGATTTATATTAAATATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAAAA

000546, 07.7301

FIGURE 96

MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKPKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFGDVKDETYDLLYQQCD
AQPASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

Downloaded from www.ascp.com

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGTTTGTGGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTTCCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCTCAGACCTGCGAGAAGCTGAAGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
TGTTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGAGC
GCGCCTGGCTGTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGCTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGCGCGAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGGCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTGTAAACCTGCCACATATCTTATTTATTCCTCCAATTCAATAAATTATTTATT
CTCCAAAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFSTLLLLASTAILNAARIPVPPACGKPPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIDSEVCSHLYWRGAGQGPTEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

0005348.071301

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCCTGCAGTTTCTGTAGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGAAGATGCTCAGGATTTGCCTTACCTGGTAAC TGAGGCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGTTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGTGTGGAACCCAGGCC
CCAACTTCCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCAAATCGACCCATGTTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCCACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGGCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTGAGCTGTCTCTCTGTCATTTCCCCACCCTGTCCCAGCCCCATAACAAGATA
CTTCTTGTTAAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCTGGAGGCACAAGGCCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCCTGAGGACTGCACACC
GGGCCCCACACCTCTCCTGCCCTCCTCTCTGAGTCTTGGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCTGAGTGCCTG
TGTAAGCTGGGATGGGGATTCCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGGAGCGAGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

09405346.071301

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPGVGTDEEKRLMVLEHNLRYRAQVSPTASDMLHMRWDEE
LAFAKAYARQCVMWGHNKERRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVWAKTERIGCGSHFCEKLGVEETNIELLVCNVEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTPTSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTVEVPSILAAHSLPSLDEEPTFPKS
THVPIPKSADKVTDKTKVPSRSPENS�DPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGDPKPSVV
SGLNSGPGHVWGPLLGLLLPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAGTGAAGTCAGGCTTTTCATTTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAGTTATAGTGGACGT
 ACTTCGTGTGTTCCCTCTGCTTGCTTTTTCACATTAGCAGACCGGACTTAAGTCACACAGATTTATCTTTCAT
 CAAGGCAAGTTTCCATGAGCCACCTTCAAGGCTTCGAGAAAGTGAACATGAACAAATGAATTTGGAGCCATTC
 AAATCTGGGACCAAGTCTCGGCAAAATATACACTTCTCTCCTTGGCTGGAAACAGGATTTGTTGAATATCTCCCTGA
 ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTCAGAGCTTCCAACTGCATT
 TCCAGCCCTACAGCTCAAAATATCTGTATCTCAACAGCAACCGAGTACATCAATGGAACTGGGTATTTTGCAAA
 TTTGGCCAAACACACTCTCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTAAACT
 GCCCACTGACCAACTCTCGAATTTGAACCGAAACAGATTAATAATGTAGATGGACTGACATTTCACAGGCTCTGG
 TGCTCTGAAGTCTGTAAGATTCGAAAGATGGAGTAACGAACCTTAGGATGGAGCTTTTGGGGGCTGAGCA
 CATGGAAATTTTGCACTGGGACCAATAACACCTTAACAGAGATTACCAAGGCTTGCTTACGGCTTGTGTATGCT
 GCAGGAATCTCACTTCAGGCCAAATGCCATCAACAGGATCAGCCCTGATCCCTGGGATCTTCGCAAGACTCAG
 TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAGACTTCTCTGGCTTGAACACTCAG
 ACTGCACATTTGGGAACAAACAGAGTCAGCTACATTGCTGATTTGTCCTTCCGGGGCTTTCCAGTTTAAAGACTTT
 GGATCTGAAGAACAAATGAATTTTCCCTGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTTGACAACTGAG
 CGCATGTGATCTCCAAGGAAATCGGATCGGTTCTATTACTAAAAAGCCCTTCACTGGTTTGGATGCTATTGGAGCA
 TCTAGACCTGAGTGACACGCAATCATGTCTTTACAAAGCAATGCATTTTCACAAAATGAAGAACTGCAACAACTT
 GCATTTAAATACATCAAGCCTTTTGTGGCATCTGCCAGCTAAATGGCTCCACAGCTGGGTGGCGGAAACAACTT
 TCAGAGCTTGTGTAATGGCACTTGTGCCATCTTCAGACTCTAAAAGGAAGAGCAATTTTGTCTGTAGCCGACA
 TGGCTTTGTGTTGTGATGATTTTCCCAAAACCCAGATCACGGTTTCAGCCAGAAACACAGTTCGGCAATTAAGGGTTT
 CAATTTGAGTTTTCATCTGCTCAGCTGCCAGCAGTGTATTCCTCAATGACTTTTGGCTGGAAAAAGACATGA
 ACTACTGTCATGATGCTGAAATGGAAAAATATGACACACTTCGGGGCCCAAGGTGGCGAGGTGTAGGAGATATACCAC
 CATCTCTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTATCTCCAATCACTTTGGTTT
 ATCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTTCAACCAAGACCCCATGGATCTCAACAT
 CCGAGCTGGGGCCATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCAGATAGCTTGGCAGAAGGA
 TGGGGGCAACAGACTTCCAGCTGCAAGGGAGAGACGATGCTGTGATGCCGAGGATGACGTGTTCTTTATCGT
 GGATGTGAAGATAGAGGACTTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTACGCAAAATGC
 AACTCTGACTGTCTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAAACCAAGGGGAAACAGC
 CGTCTTCAAGTGCATTGCTGGAGGAAGCCCTCCCTTAACTGAACTGGACCAAGAGATGATAGCCCATTTGTTGTT
 AACCGAGAGGCACTTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGTGCTGGGAA
 ATACACATGTGAGATGTCTAACACCTTGGCACTGAGAGAGGAAACGTTGGCCCTCAGTGTATCCCCACTCCAACT
 CTGCGACTCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGC
 CGTGGTTTGTGCTGTGGTGGGCAGTCACTGCTGTGGGTGGTTCATCATATACCAACAAAGGCGGGAATGAAGA
 TTGACAGATTAACCAACAGATGAGACCAACTTGCACAGCAGATTTCTCAGTATTTGTCAATCTCAGGCAAGCTT
 AGCTGACAGGCGAGGATGGACGCTGCTTCAGAAAGTGAAGCCACACCACTGATTTGTGATCATTGAGTGTCTGGT
 ATTTTCTTACCACTCAATGTGACAGTGTGGGACCTGCCATATTGCAATAGCAGTGAAGCTGATGTGGAAGCTGC
 CAGAGATGTGTTTCTTTCGCTTTTGGGATCCACAGGCCCTATGTATTTTGAAGGGAATGTGTATGGCTCAGCA
 TCCCTTTGAAACATATCATACAGGTGACGCTTGCACGACAGTATTTGATGAGCACTATGAGCCAGTATTA
 CATAAAGAAAGAGAGTGTACCCATGTTCTCATCTTCAGAAAGATCCTGCGAAGCGAGCTTCAGTAATATATC
 GTGGCTTCACTGTGAGGAGAGCTTTAACACTAGTTACTCTCAATAGAAAGCTTGAATGAAAAATCTGTG
 TCTAAACAGTCTCTTTAGATTTTACTGCAAACTCAGAGCCAGGCTCGGTTGGCTCGAGTATTTCTTTCATGGG
 TACCTTTGGAAGAGCTCTCAGAGAGACTCACTAGATGCCATTACAGCTTTGGACAGCCATCAGATGTGCGCC
 AAGAGCCCTTTTATTTGAAAGCTACTTCCCCAGCACTTGGACTCGGTCGAGGAAGATGGGAAGAAAGGAC
 AGATTTTCAGGAAGAAAAATCACATTTGTACTCTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGT
 TTTATGATCTTGACACATAGACTGTAATGAGACCAAGGAAAGCTTAACTACTACTCCTCAAGTGAACCTTTATTTA
 AAGAGAGAGAACTCTTATTTTAAATGGAGTTATGAATTTTAAAGGATAAAAATGCTTTATTTATACAGAT
 GAACCAAAATTAAGAAAGTTATGAAAAATTTTATACCTGGGAATGATGCTCATATAAGAAATCCTTTTAAACTA
 TTTTTTTACCTTTGTTTGTGCAAAAGATCTTATCGTAAATTAATGATATGAATTTATTTATTTATGATTT
 TTTATATGCCAGATTTCTTTTATGAAAAATGAGTTACTAAAGCACTTTAAATATACTCTGCGCTGTACCATTTT
 TTAATAGAGATTACTTCAATATATTTGCACTATATTTAATAAAATGTCATTTGGA

09505346.071301

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRISAIPPKMFKLPLQLQHLLELNRRNKIKNVDLGLTFQGLGALKSLKM
QRNGVTIKLMDGAFWGLSNMEILQLDHNNLTETIKGWLYGLLLMQELHLSQNAINRISPDawe
FCQKLSLELDLTFNHL SRLDDSSFLGLSLLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSIKKKFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNNTSLLCDCQLKWLQWVAENNFSQFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFAGEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTTKTPMDLTIRAGA
MARLECAAVGHAPAQIAWQDKGGTDFPAARERRRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPFPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSVDSDAGKYTCMSNTLGTGERGNVRLSVIPTPCDSPQMTAPSLDDDG
WATVGVVVIIVVCCVVGTSLVVWVVIIVHTRRRNEDCSIINTDETNPADIPSYLSSQGTAD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSTCHIDNSSEADVEAATDLFLCPLGSGTGP
MYLKGNVYSGDPFETYHTGCSPPDRPTVLMHDHYEPSYIKKKECYPCSHPSSESCERSFSNLSW
PSHVRLKLNNTSYSHNEGPMKNLCLNKSSLDFSANPEPASVASSNSPFGTFGKALRRPHLDA
YSSFGQPSDCQPRAPYLKAHSSPDLDGSGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTTTGGGTGCTTGCAAAAAATG
AAGGATGCAGGAGCGCAGCTTTCTCCTGGAAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAGAAGGAAGAAC
GAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCCAGAGTTAGACCCGCGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
CCACCCCAAAAAAAGGATGATTGGAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTCTATTTTTCTC
TATAAAGGAGAAAGTTGAGCCAGGAGATATTTTGGAAATGAAAGTTTGGGGCTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTCTTTCTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAACATCTGCAAAAGAAA
TTTCAGAGAGAAAAAGTTGACCCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCCAGCAGAGCAGATTGGA
TTTGTGCTATGTGTACTAAAAATGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTAAAT
TTTTATTCCTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACCACTCGGATTCCATCTGGATGTTGGT
TGATCAGCTGTAAGATACACTGTTTGAATTCAGAAGGACCAACACAGATAAATTAATGAATGTTGAACAAGAT
GACCTTACATCCACAGAGATAATGATAGTCTTAGGTTTAAACAGGCCCTATTGACCCCTGCTTTGTGTGCT
GCTGGCTCTTCACTTCTTGTGGTGGCTGGTCTGTCGCGCTCAGACCTGCCCTCTGTGTGCTCCTCGACGAA
CCAGTTCCAGCAAGGTGATTGTGTTCGGA AAAACCTCGCTGAGGTTCCGGATGGCATCTCCACAACACACGGCT
GCTGAACCTCCATGAGAACCAAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGATATACTGTCTAAACTGAAGGAGCTCTGGT
GCGAAACAACCCCAATTGAAAGCATCCCTCTTATGCTTTAACAGAATTCCTTTTTCGCCCGACTAGACTTAGG
GGAATTGAAAGACTTTCATACATCTCAGAAGGTGCCCTTGAAGGTCTGTCCAACCTGAGGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
TTTATCTGCCATCAGGCTGGCTCTTCCAGGGTTTGTATGACCTTCAAAAACTGTGGTGATACAGTCCAGAT
TCAAGTGATTGAACGGAATGCCCTTGACAACTTCAGTCACTAGTGAGATCAACCTGGCACCAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTACATCACACCCCTTGAACCTG
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG
TAACTACTCCTCCCAATCTAAGGGGAGGTACATTGGAGAGCTCGACAGAAATTACTTACATGCTATGCTCCGCT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCCGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGCGTACAAAGTGCAGTAGCTGT
GCTCAGTGATGGTACGTTAAATTTACAAATGTAACTGTGCAAGATACAGGCTGTACACATGTATGGTGAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCACTACTCTCTTCTCTTACTTTTC
AACCCTCAGACTAGAGACTATGGAACCGTCTCAGGATGAGGCAAGGACACAGATAACAAATGTGGGTCCCCTCC
AGTGGTGCAGCTGGGAGACCACCAATGTGACCCTCTCTCACACACAGAGCAAGGTGCGACAGAGAAAAACCTT
CACCATCCAGCTGATGATATAAACAGTGGGATCCAGGAATTTGATGAGGTCAATGAAGACTACCAAAATCATCAT
TGGGTGTTTTGTGGCCATCACACTCATGGCTGAGTGATGCTGCTCATTTTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCAGCCCCCAAGGACTGTTGAAATTAATATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCACTGCCCATGCCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
CAACACACACAAACAGTTAAACACATAAATTCAAATCAACAGTTCAGTGACATAAACCCTTATTGATCCGAATGAA
CTCAAGACCAATGTACAGAGACTCAAACTTAAACATTACAGAGTTTACAGAAAAACAACAAATCAAAAAAACA
ACAGTTTATTAATAATGCACAAATGACTGGCTAAATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACA
AAAGAAAAGAAATTTATTTATTAATAATCTATTGTGATCTAAGCAGACAAAA

000543.071301

FIGURE 104

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPVSCSCSNQFSKVIC
VRKNLREVDPDGISTNTRLLNLHENQIQIIVKNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNRLRYNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAPFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVGN
TTASATLNVTAATTTTPFSYFSTVTIVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTFQ
STRSTKFTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHHRQN
HHAPTRTVEIINVDDDEITGDTMPESHLPMPAIEHEHLNHNYSYKSPFNHTTTVTNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCGCAGCGTGCTCAAGCTGCAACTCTGTTGCAAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCGCCGCCGGGAGTTAAAGAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCAGCGCAGCCG
GAGGGCGGGCTTCACCCTTCGGTTCGGTGAAGTTTGTCCGGGCCCGAGCGCGCGCGGTTCGGGAGCTTCGGGTAGA
GACTAGGCCGCTGGACCGCGGCTAGAGCGCGCGAGCCCTCGTGCAGCGCGCGCGGGGTTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGGCGCGCTGCCCGGTCCGACAGCGCGGCTCGCGGGAACTCGGGCAGCCCTTCGGGTAGCGCGC
GAGCGCCATGCCCACTACTCGTCCGCTGCCTCGGGGACCTGCTGGACTCGACTCGTAAGCGGCTAGCGCGTCTTC
CCCGAGCCACTTCGCTTCGGGTGCTCGGCTGGACTTAAGTACAAACAGATTATCTTTTCATCAAGGCAAGTTCC
ATGAGCCACTCTCAAAGCCTTCGAGAAGTGAACACTGAACACAAATGAATTTGGAGACCATCCAAATCTGGGACCA
GCTCTGGCAAAATATACACTTCTCTCTTGGCTGGAAACAGGATTGTTGAACACTCTCCCTGAAACATCTGAAAGAG
TTTCAGTCCCTTTGAACTTTGGACCTTAGCAGCAACAAATATTTAGAGCTCCAACTGCAATTTCCAGCCCTCAGC
CTCAAATATCTGATCTCAAACAGCAACCGAGTACATCAATGGAACTGGGTATTTTGACAATTTGGCCAAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCCAAGATGTTTAACTTGCCCCAACTGCA
CATCTCGAATTGAACCGAAACAGATTAAAAATGTAGATGGACTGACATTCGAAGGCTTGGTGCTCTGAAGTCT
CTGAAATGCAAGAAATGGAGTAAAGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCAATAACAACTAACAGGATTACCAAGGCTGGCTTTACGGCTTGCTGATGCTGAGGAACTTCAT
CTCAGCAAAATGCCATCAACAGGATCAGCCCTGATGCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAACTACTTCAAGGCTAGAGATTCAAGCTTCCTGGCCTAAGCTTACTAAATACACTGCCACTTTGGG
AACACAGAGTCAGCTACATTTGCTGATTTGCTCTCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTCCTGGACTTATTGAACATGAATGTGCTTTCTCGGGCTTGACAACTGAGCGAGCTGACTACTC
CAAGGAAATCGGATTCGTTCTTATTACTAAAAAGCCCTCAGCTGGTTGGATGCTTGGAGCATCTAGACCTGAGT
GACACAGCAATCATGTTCTTCAAGGCAATGCATTTTCAAAATGAAGAAACTGCAACAAATGCAATTTAAATACA
TCAAGCCTTTTGGGATTTGCCAGTCAAAATGAGTTCCCAAGTGGGTGGCGGAAACAACTTTAGAGCTTTGTA
AATGCCAGTTGTGGCCATCTCAGCTGCTTAAAGGAAGAAAGCAATTTTGTGCTTAGCCCGAGATGGCTTTGTGTG
GATGATTTTCCAAACCCAGATCAGGTTTCAGCCAGAAACACAGTGGCGAATAAAGGTTCCAAATTTGAGTTGT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGTCTGGAAGAAAGCAATGAATCTGCTGATGAT
GCTGAAATGGAATAATATGCACACTCCGGGGCCAGGTGGCGAGGTGATGGAGTTATACCAATCTCTCGGCTG
CGCGAGGTGGAATTTGCGAGTGGGGGAAATATCAGTGTGTCATCTCCAATCACTTTGTTTCATCTCTACTCTGTC
AAAGCCAAAGCTTACAGTAATATGCTTCCCTCATTCACCAAGACCCCCAGATGCTCACCATCCGAGTGGGGGCC
ATGGCAGCTTTGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGATGCAATGTGATGCCCGAGGATGACGTGTTCTTATCTGGGATGTGAAGATA
GAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGATTATTCAGCAAAATGCAACTCTGACTGTC
CTAGAAACACCATCAATTTTTCGGCCACTGTTGGACCGAACTGAAACCAAGGGAGAAACAGCCGCTCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCATTGTTGTTAAACCGAGGAC
TTTTTTGGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACACATGTGAG
ATGTTACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGATGATCCCACTCAACCTGCGACTCCCT
CAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTTGCTGTGCTGT
GTGTTGGGCACGTCATCTGTGGTGGTGGTCATCATATACACACAAGGGCGGAGGAATGAAGATTGCTGAGCATACC
AACACAGATGAGACCACTTGCACGACGATATTCCTAGTTATTGTCATCTCAGGGAACTGGATGTCACAGGCAG
GATGGTACGTTCTTCAGAAAGTGGAGCCACCCAGTTTGTCACTCTTCAGGTGCTGGATTCTTTCTACCA
CAACATGACAGTAGTGGGACTTGCATATTGACAATAGCAGTGAAGCTGATGTCAGGCTGACCAAGATCTGTC
CTTTGTCGTTTGGGATCCACAGGCCCTATGTTATTTGAAGGGAAATGTGATGGCTCAGATCTTTTGAACACA
TATCATCGCTGTCAGCTGCTGACCAAGAACAGTTTAAATGGACCACTATGAGCCAGTTACATGAAGAAAAAG
GAGTGTACCCACTTTCTCATCTTCAGAGAATCCTGCGAACGAGCTCAGTAATATATCTGTGGCTTCACAT
GTGAGGAGCTACTTAACTCAGTTACTCTCAATGAAGGACCTGGAATGAAAAATCTGTGTCATAACAGAGTCC
TCTTTAGATTTTGTGCAAAATCCAGAGCCAGCGTGGTTGCTCAGTAATCTTTTCATGGGTGATTTTGGAAAA
GCTCTCAGAGAGACTCAGCTAGATCTGCTTCAAGCTTTGACAGCCATGATTTGCTCAGGACGAGCTTTTAT
TTGAAGCTCATTTCTCCCGACACTTGGACTTGGGTGAGAGGAAGTGGGAAGGAAGGACAGATTTTCAGGAA
GAAATTCAAATTTGACTTTTAAACACAGCTTGAAGAACTACAGGACTCCAAATTTTCACTCTATGACTGGAC
ACATAGACTGAATGAGCAACAGGAAGCTTAACTACTACCTCAAGTGAACCTTTTATTTAAAGAGGAGAAAT
CTTATGTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAATGCTTTTATACAGATGAACCAAAATAC
AAAAGTTATGAAATTTTATACCTGGGAATGATGCTCATATAAGAAATACCTTTTAAACTATTTTAACTTTG
TTTTATGCAAAAAGTATCTCATGTAATTAATGATAAATCATGATTTTATGATTTTATATGTCGACA
TTCTTTTATGAAAAATGAGTTACAAAGCAATTTAAATAATACCTGCTTGTACCATTTTAAATAGAAAGTT
ACTTCATATATTTTCACATATATTTAATAAAATGTGCTCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

09305348.071001

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLDCSR
 KRLARLPPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
 LLSLAGNRIVEILPEHLKEFQSLLETLDLSSNNISELQTAFFALQKLYLYLNSNRVTSMEPGY
 PDNLANTLLVLKLNRRNRI SAIPPKMFKLPLQLHLELNRRNKIKNVGDGLTFQGLGALKSLKMQR
 NGVTKLMDGAFWGLSNMEILQLDHNRLTEITKGWLYGLLMLQELHLSQNAINRISPDWEFC
 QKLSRLDLTFNHLRLDDSSFLGLSLLNLT LHIGNRVSYIADCAFRGLSSLKTLDLKNNNEIS
 WTIEDMNGAFSGLDKLRRLILQGNRIRISITKKAPTGLDALEHLDSLDAIMSLQGNAFSQMK
 KLQQLHLNLTSSLLCDCQLKWLPPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDFF
 PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLDHAEMENYAHLRAQGGGE
 VMEYTTILRLREVEFASGKYQCVISNHFSSSYSVKAKLTVNMLPSFTKTPTMDLTIRAGAMA
 RLECAAVGHPAPQIAWQKDGDTFFAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
 GSISANATLTVLETPSFLRPLLDRTVTTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF
 FAAGNQLLIIVSDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
 TVGVVIIAVVCCVVGTSLVVVVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTADRQ
 DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCCHIDNSSEADVEAATDLFLCPFLGSTGPMY
 LKGNVYGSDPFETYHTGCSPPDRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS
 HVRKLNTSYSHNEGPGMKNLCLNKSSLDPSANPEPASVASSNSFMGTGPKALRRPHLDAYS
 SFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQEBENHICTFKQTLNRYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
 688-692, 729-733, 956-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

0905348-071301

CAAAACCTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAGAGAGCCGAGCCCGCGGAGCCGACGCTAGACAT
TGGGGGAGCGCGCTTTCGCGCTTGTTGGGCGCGCTCGGCGCGCCGAGCAGGAGGGAAGCTTGTTGCTCTCC
CTGCTTCCACGAGGCGCACTGTGTGTAACGGGAGAGCCCTGGTGTGCTCCGCTCCCTATCCCTCCCTTTATATA
GAAACCTTCCACATCGGGAAGAGCAGCGGAGGAGCGAGGCGCTCATGTGTGAGCAGAAAGGCGCGGCTGATCTGCG
GCGCACAGCATTTCCGAGTTTACAGATTTTTACATACAAATGTCAGGCGAGGAGGCAGAACAGCTCTCCGGT
TCGATCAGCCCTCGGGCCCGCAGCGCATCTGACTGACCTGACCCCTTCAGGCACAGATGGCCAGGACCGGGGTGTG
TGCTCTCGTCTGCTGCTGCGCGCACTGCTGACCTGGAGCATCTGTGCTTGTGCGTAGGAGGCGCAGGATTTGGCGCGA
GTGGGCGCGCACAGCTGAGCCCGCGGAGAGCAATTTTCGGAAGAGAGACCGGTGTCTGGTATGAGCCCTGAG
AGCCGGGCGCTGGCCAGCCGCGCTCAGCTGAGCCCGAGACTGTGCTCTTCGCGAGGAGGCGTGTGGAATCTG
GCGGATTTGACCTCGGTGAGTTTCGCGGGGAGCTGCTGTAGACACACAAACCATCTCTTCAGAACAAACAGC
TGAAAAGATCTACCTCGAGGAGCTTCTCCGGCTGCACCGGCTGTGAGACATGAACTCGACAAACACCGCTGTA
CTTCCGAGGGCTCCAGAGAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTTCGCAATACAAAG
TGACCTTGGCACCCCGCTTCCTGCGAAACGCTGATCAGTGTGGAATTTGCTGSCAACTATGCTCCACGAATCT
ATGGGCTCACTTTGGCCAGAGCCAAATCTGAGGCTGTGTGTAACCTGCACAAACAACTGGCAGACCGCGGG
TGCCGACACATGTTTCAACGCTCGACGAGCTCGAGGTCTCTACTCTGTTCAGCAAGCTCTGCGCGACCTGTG
CCAAAGACCTGCGGCTGCGCTTGTACAGAGCTGCACTCAAGAACACAAAGCTGAGAAGATCCCCCGGGGGCT
TCAGGAGCTGCAGAGCTTCGCGAGCTATACCTGCAAGAACACTACTGTACTGACGAGGGGCTGGACACAGGA
CCTTCTGGAAGCTCTCCAGCTTGGATGATCTGATCTTCCAGCAACCAACTGTCTCGGGCTGAGAGCTGGGCTGCG
CGCGAGCTGTGCTGCTGCACTTGAGAAGAACGCCATCCGAGAGCTGCCAGTGTGCTGACCCCCCTCG
CGAGCTTGGATCTCTGCTGTCGACAGAACCTCGGGAGCAGGGCATCCACCTCGGCTTCTCGAGGCC
TCAAGCGTTTGACACCGTGCACCTGTACACAAACCGCTGAGCGCGTGCCAGTGCGGCTCTCGCGCGCTGTC
TCACCTCATGATCTTCCACACCAAGATCAGGAGCATTTGCCCGAGAGATTTGCCACACCTACTCTCTGGAG
AGCTCCAGCTCAGCTACACCGCATCACCAGCCACAGGTGACCGGACGCTTCCGAGAGCTGCGCTTCTGTG
GCTGCTGAGCCTGTTCGGCAACCGGCTGCACACCTGCACTGGGCTGCTCGAATGTCCATGTGCTGAGG
TCAAGCGATAGTGAAGTCTGCTGCTTGGCACAGGGGGCTTCGGGCGTACGCTGCTGTGAGCTTACTCTCA
CCAGAACCGATCGCTGCGCAGGAGCTCTGGCCCGCTGCTGGGTGAGCATCGCCATCTGCAGCTCTGCGACA
TGCGCGGGAATCAGCTCAGAGATCTCCCGAGGGGCTCCCGAGCTCACTTGATGACTGTACTCGACAAACACA
AGATTGCTGCGGTGCCGCCCAATGCTTGAATCTCAGCGACCTCAGAGGATCTTTCTCAGTTTAAACAG
TGCTGTGGGCTCGTGGTTCGACACATGCTCTTCGGAGGCTGAAGCACTTCAGACTTTGACATGGAAGCACT
TAGAGTTTGTGATCAATTGCAAGCACGGTGGCGCTTTGGGAGAGGAAAGGAGGAGGAGAGAGAGAGACAGGAC
AGGAAGAGGAAACAAGATAGTGAAGCAGAGGTATGACAGTGTGACTTAGGATGTGAGCCCGCGACTCTTTCG
ACAGACACGCTGTGTGCTGTGAGCCGCCATCTCTCGGTGCTGCACAGACACACAGGCTGCACATGTAGGCA
TCCCACTGACAGCGGCTGACACGCTCTATATCCCACTCTCCAGCGGTGTCACCGGACAGCATGCG
ACACACATCACACCTCAAACAACAGCTCAGGCCACACACAACCTCAACCAACACAGCTCTCTGTACAC
CCCCATACCGCTGCACCGCTCTGAAATCTGACATGCAGGAGGGTTCGCCCTGCCCTGGGCACACAGGCCACCA
TTCCTCCCCCTGTGATCATGTGTATGCGTAGTCATACACACACACACATCAGTCACTGTGTGGA
CAGCCCTCAAAGGCTGATCCGACACAGACTCTTCGCGAGCAGATCAGCTATGACACTCGCGCTCGCCCT
GTGATCTTGTGCTGCTGTTCTCGTAGAAGACACAGGSETCATGCTCTGTGGCAGGCTGCTTGCACCTCT
GGAATCACAAAGGCTGAGTTTATTTCTCTTCCATCTCATGGGACAGAGCGCTCAGAGATGCTGGGCTGCC
TGGCCACCTGCTCTTCGAGTCTGTGGGAGTCACTCTGTAGAGTCCCTTCGCGCACGCCCTGCGGAGCA
CAGGCATTTTCCATAGGAGGACCGCATGTGAGGACAGTAGGAGAGCCCTGGTGTGCTGTGGGCTTGGG
CAGGATGTGAACGAGGATGATGGGCTGGGCTGAGCAGGAGGAGGACCGAGCTGACCTGAGAGACACTTT
GTTCTTCAGGCTGTGGGGGAAGTTGAGGGGCTAATTAATTAATTTTATCTTTTAAAGGAAAAATATAAAAT
CTCAAGCTGATTTTTCTTGTATTCGAAAGAACTTAATAAAGATTAATCCCTATCCCTCGCGAAAAA

FIGURE 108

MEGEEAEQPAWFHQPWPRPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSP EENEF AEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVD CGGIDLREFPGDLP
EHTNHLSQLNNQLEKIYPEELSR LHRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLR SVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSIRELYLQNNYLTDEGLDN
ETFWKLSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHNSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

Downloaded from www.ascp.org

FIGURE 109

GGGAGGGGGCTCCGGGGCCGCGCAGCAGACCTGCTCCGCGCGCGCCCTCGCCGCTGCTCTCCGGAGCGGGCAG
CAGTAGCCCGGGGGCGGGAGGGCTGGGGGTTCTCTCGAGACTCTCAGAGGGGGCGCTCCCATCGGCCCAACCACC
CAACCTGTCTCCGCGCGCACTGCGCTGCGGCCAGGACCCGCTGCCCAACATGGATTTTCTCTGGCGCTGGT
GCTGGTATCCTCGCTCTACTGCAAGCGCGCGCGCGAGTTCGACGGGAGGTGGCCAGGACAAATAGTGTATCGAT
TGGCCTATGTCTGTTATGGTGGGAGGATTTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTTGGGGACAGTGCAGCC
TGTGTGCCCAACACAGATGCAAAATAGTGAATGTATCGGGCCAAACAGTGCAGTGTCTCTGGTATGCTGG
AAAAACCTGTAAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCGGCCCTGTGAAGCACAGGTGCATGAACACTTA
CGCGAGCTTACAGTGTCTACTGTCTCAACGGATATATGCTCATGCGGATGGTTCCTGCTCAAGTGGCCCTGACCTG
CTCCATGCGAAACTGTGAGTATGGCTGTGATGTTTAAAGGACAAATACGGTGAAGTGCATCCCTGGCCCT
GACCTGGCTCCGTGAGTGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCCTCGCCCTAGATT
TAGCCAAATGTGTCAACATCTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTGTATTTGGAGG
CAAATATCAATGTCTAGCAGTAGACGAATCCTCACTTGGTCACTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCTACAAGTGCAATGTAAAGAAGGATACACGGGTGATGGACTGACTTGTGTGTATATCCCAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGAAA
TAATAATTTGGATTCTGTGATTTGGAGTACTTGGTGGCTCCGAAGACACCATATATCTCTCATCTATACCAA
CAGGCTACTCTTAAGCGCAACCAAGACCTACACAAAGCCACACCAATTTCTCACTCCACACCAACCACCC
CTTGCCCAACAGAGCTCAGAACACCTCTACCACTTACAACCCAGAAAGGCCAACACCCGAGTGCACACTATAGC
ACCAGCTGCCAGTACACCTTCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGACCTCAGAAAAACCCAGAG
AGATGTGTTTCAGTGTTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAAATATCTGACAGTGTCCGCGCAGAAAGCCGAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCAATTCAGGGGACCTGTGCTGTCTTCAAGGCA
CAAGGTGACGGGGCTGCACCTCTGGCACACTCCAGGTGTTTGTGAGAAAAACCGTGGCCACGGAGCAGCCCTGTG
GGGAGGAAATGGTGCCATGGCTGGAGGCAACACAGATCACTTGGCGAGGGCTGACATCAAGAGCGAATCACA
AAGATGAATTAAAGGGTTGGAAGAAAGATCTATGATGGAAAAATTAAGGAACTGGGATTATTGAGCTGGAGAG
AGAAGACTGAGGGGCAAAACCATGATGTTTCAAGTATATGAAGGGTTGGCACAGAGGGTGGCGACAGCTGT
TTCTCCATATGCACTAAGAAATAGAACAGAGGAACTGGCTTAGACTAGAGTAAAGGAGCATTTCCTTGGCAGG
GGCATTGTAGAACTCTATAAAAAAGAGTGTGAAATCTCAGTATCTCTCTCTTTTCAAAAAATTAGA
TAAAAATTTGCTATTTAAGATGGTTAAAGATGTTCTTACCAGGAAAAAGTAAACAAATTTATAGAATTTCCAAA
AGATGTTTGTATCTACTAGTAGTATGCAAGTGAATCTTTAGAACTAAATTAATTTGGACAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGATTGAAGGGGGAAGGCCACCAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAGAAAAAGGAAACTATTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTCATTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAAGAGCTCTTCAAGGAACAGATTACAGAGC
ATTTTCAGGTGCAATCTCTCTCTCTGCTGTGTGACAAAGTATCTTGGCTGCTGAGAAGAGTGCCTGCCCC
ACACCGGACAGCTTTCTTCACTCATCAGTATGATTCAGTTTCTCTTATCAATTTGAAGTCTCCACAGGTCCAC
AGAACCTGAATATTTTTCACCTATAGGTACAAATAGAGGTCTTCTGTCAATTTCTGTAAGTGCCTGAGTGGCTGG
AGGGGGAAAAATAATCAATAGCCCTTTGAGTAACGGCAGAAATATATGGCTGTAGATCCATTTTAAATGGTTCATT
TCCTTTATGCTCATTAAGTGCAGCTGAAGTGAAGGGGAAAAATAATGAAATTTTCTTTCATGTGCCAA
TGATACATTTGCACTAAACTGATGGAAGAAATATCCAAAGTACTGTATAACACTCTGTTTATATTTAAATGTTT
CTAAAAATAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAACAATTTATTTGTAATAAAAAACATGTTAGTAA

CG003748.071301

025053+301 = 027301

Signal sequence:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCAATTGCCCCCTTAGATTGTGA
AATGTTGGCTCAAGGTCCTTCACAACTTTCTTCTTTCGCAACAGGTGCTTGCTCGGGGCTGA
 AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
 CACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGTACTTGGAAATACC
 AACACAAGTTACCATGATGCGCACCCAATGCATCTGTCTTATCAACCCACTGCAGTTCCTT
 GATGAAGGCCATTACATCGTGAAGGTCAACATTTCAGGGAAATGGAACCTATCTGCCAGTCA
 GAAGATACAAGTCACGGTTGATGATCCTGTGCACAAAGCCAGTGGTGCAGATTTCCTCCCT
 CTGGGGCTGTGGAGTATGTGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
 CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
 TCCCCAAAACAATACCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
 GCCTGGTGAGGAACCTGTGCAGTGAATGGAAAGTGATATCATTATGCCCATCATATATTAT
 GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAAGTAGGGGAAGTGTTTACTGT
 TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACTACT
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCCTCGCTTAGAAGTT
 GCATCTGAGAAAGTAGCCCGAGAAGCAATGGACTATGTGTGCTGTGCTTACAAACAATAAC
 CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
 CACGAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATT
 ATATCCATGTGTCTTCTCTTCTATGAAAAAATATCAACCTTACAAAGTTATAAAAACAGAA
 ACTAGAAGGCAGGCCGAGAAACAGAATACAGGAAAGCTCAAAACATTTTCAGGCCATGAAGATG
 CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTCCAGATGTTTCTGGTGTTCACAGG
 ATTCCAAGCAGGCTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
 GTATGAAGTTATTCAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTCATGG
 GCTAAACAGTACATTGAGTGAAATTTGAAAGAAACATTTTAAAGGAAAAACAGTGAAAAAGT
 ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACCTCTTACTCATTTATCTCTTTTACA
 TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACAAATGTCTT
 GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
 GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTGTATGAAATATCTCTACAAACCTCA
 ATTAGTTTCTACTCTACACTTTCATATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
 TGTGGAACTTTACATTGTTTCGATTTTTCAGCAGACTTTGTTTTTAAATTTTATATAGTG
 TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTGTTTATTGTACAA
 CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC
 AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAGCTCTTTTTTTA
 TTTTTTTTCAAGGAAAGATGGATTCAATAAATATTCTGTTTTTGCCTTTTAAAAAATAAAAAA

0905348.071301

FIGURE 112

MWLKVFTTFLSFATGACSGLKVITVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYL LGSVNKSVVPDLEYQHKFTMMFPNASLLINPLQFPDEGNYIVKVNIQNGTSLASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGCGGAAATGCGGCCCTCCGGGAGTCTTGCAAGTTCCCTGGCAGTCTGGTGCTGTT
GCTTTGGGGTGCTCCCTGGAGCGCACGGGCGCGGAGCAACGTTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGGCTGAATGGGGAGAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCAAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCTACTATTTATCATTGTAAGATGGTGAATTTAGGCGCTATCAGGTCGAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAGAGATTTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCTTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAAGAAGAAGCTGAAAGTAAAGAAGGAACAACAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTTGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATATTGATTTTGATAAAAACAGAAGATTGATCATTTTGTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAAGGTTTCAGTCTAGATTGTCAATTAATGAAGAGTCTA
CATTGAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTGA AAAAATCGTGCCAAGCAATAAGATTATGTATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTGA AAAATTTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTGATATAATTTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTCACTGACAATTTCTGGTCTTTTTAGAGGTATATCCAAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATACAGTTTCTTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTAAGTTCATGTTATCTCTTGATTC
CAACAAAGTTTGATTTTTCTCTGTATTTTCTTACTTACTATGGGTACATTTTTTATTTTT
CAAATTTGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGT
GTTTCAAACGAAAGTTTACTGAGAGATCCATCAAATGAACAATCTGTTGTAATTTAAATTT
TTGGCCACTTTTTTCAGATTTTACATCATTCTTGCTGAACTTCAACTTGAAATTTGTTTTTT
TTTTCTTTTTGGATGTGAAGGTGAACATTTCTGATTTTTGTCTGATGTGAAAGCCCTGGTA
TTTTACATTTTGAAAAATTCAGAGAAAGCTTAATATAAAAGTTTGCAATTTACTCAGGAAAAAG
CATCTCTTGTATATGTCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTTAAAAATAATAACATTTTTATATTTTTTAAAGACAA
ACTTCATATTTACTCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTACAGGTAAAA
GTCAGTAGGATGGAACATTTTAGTGATTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAAGGGGAAAAATCATAAATACAATGAATCACTGACCATTACGTAGTAGAC
AATTTCTGTAATGTCCCTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAAATTTAAATATTGTACCATT
AAAGATTTGGATGTGTTAACTTGTGATGCCCTAGAAAAATATCCTAAGCACAAAATAACCT
TTCTAACCACTTCATTAAAGCTGAAAAA AAAAAAAAAA

0005348.071301

FIGURE 114

MAPSGSLAVPLAVLVLLWLGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

102540.045060

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCTT
 CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
 AAGGTCCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
 ATTGCTGATGGCTCGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACTCTATTG
 GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
 CTTGTGGAGGAAGCCAAAGCTTTCCAAGATTAAAGAGCTGGGCCAACAAAAATGGAAGCCTTGAC
 TAGCAAGTCAGCTGCTGATGTCTGAGGGCTACCTGGCTCACCTGTGAAATGCCTACAAACTGG
 TGAAGCGGCTAAACACAGACTGGCCCTGCCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
 GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCACCTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
 GAGGGGAACCTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTTGTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATGCCCGGGGAGGGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGTGACCGTGCCCTGGAGCTCACCCGCGCCTGCTC
 TCCCTTGACCCAAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
 TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGTCTGGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
 CAGGGCCCCACAGCTGCTCATTTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
 TCGTCAGGTACTACGATGTCTATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCTACTGTCTGCCAGCTA
 CCGGGTTTCCAAAAGCTCCTGCGCTAGAGGAAGATGATGACCTGTGTGGCCCGAGTAAATC
 GTCGGATGCAGCATATCACAGGGTTAAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAAT
 TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGAAGCGG
 CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
 GTGGTGCCACCGTCTTCCCTGATCTGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
 TTCTGGTACAACCTCTTGCAGGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCCTGCCC
 TGTGCTTTGGGCTGCAAGTGCGGTCTCCAATAAGTGTTCCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACTGAATCATCCTTTTCTGTCTTCCCTTCCCTGGGT
 CTTACGCCCATGTCAACGTGACAGACACCTTTGTATGTTCCCTTTGTATGTTTCCATCAGGCT
 GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
 GTGACTGAAGTCCCAGCCCTTCCATTACGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
 AAGTGGCTGCAGCAGATTAGCTGTCTAGCGCCTAGCAAGGTGCTTTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTTCAGTGAACCAAGTCTGATACCTTGTTACATGTTTGTGTTTTAT
 GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

0905348.071301

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAALMRLQDITYRLDPGTISRGEPLGTYQAMLSVDDCFGMGRSAYNEGDIYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEREKTLTNQTEAELATPEGIYERPDVYLPERDVYESLCRGEVGLTPPRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDPS
RRPFDGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTCTTTTAGTGGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATGTT
TTCATTATTACCGTTTGGGTGGGGGTTAGTTCGACACCTTTCACAGTTGAAGAGCAGGCAGGAAGAGTTGTGA
AGACAGGACCAATCTCTTGGGGATGCTGGTCTGGAAGCCAGCGGGCTTGCTCTGTCTTTGGCCTCATTGACCC
CAGGTTCTCTGGTTAAATCTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATGATCCTTGAGGCTGTGCC
CCTGGGGCACCACCTGGCAGGGGCTTACACCAATGCGACTGAGCTCCCTGTTGGCTCTGTCTGGCGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGGTGAGCCTTGAGCCTCCTGTGGGTTTCCCTGGATCAGGGGGAGGGGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCAGGAGGGGCCACAGAATCCAGATTCCAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAAACCCGGATTGTCCCTACTACAGGGACCCCAACAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAAGCGTTGCTGGTGGCTGTCTGACCTCCGAGCTACACTGTCCA
CTTTGGCGGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTACTCTACTTCACTGGGAGCGGGGG
CCCGGGCTCCAGCAGGATGCAAGTGGTGTCTCATGGGGATGAGCGGCCCGCTGGCTCATGTGAGAGACCTGCG
GCCACCTTCAACACACACTTTGGGGCGACTACGACTGGTCTTCATCATGAGGATGACACATATGTGAGGCC
CCCGCTTGGCAGCCCTTGCTGGCCACCTCAGCATCAACAAAGACCTGTACTTAGGCGGGGAGAGGAGTTCAATTG
GCGCAGGCGAGCAGGCCCGGTACTGTCA TGGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGTCTCGTCTGC
GGCCACATCTGGATGGCTGCCGAGGAGACATTTCTCAGTGCCGCTCTGACGAGTGGCTTGGACGCTGCCTCAATTG
ACTCTCTGGGCGTCGGCTGTGTCTCACAGCACAGGGGCGAGCAGTATCGCTCAATTGAAC TGGCCAAAAATAGGG
ACCTTGAGAAGGAAGGAGCTCGGCTTTCCTGAGTGCTTCGCGGTGCACCTGTCTCCGAAGGTACCTCATGT
ACCGGCTCCAACACGCTTCAGCGCTCTGGAGTTGGAGCGGCTTACAGTGAAATAGAACAACTGCGAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCGAAGGGGAGGCGAGGCTGAGCTGGCCGTTGGGCTCCCTGCTCCTTTCA
CACCACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCTGTGCAGATGGGG
CTCCCAAGTGCCCACTACAGGGGGTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGCTATCAGCCCCGCTCGCCTTCCAGAAGCAGCGACTGTCTCAACGGCTATCGGCGCTTCGACCCAGCAC
GGGCGATGGATACACCTTGGACCTGTCTGTGGAATGTGTGACACAGCGTGGGCACCGCGGGCCCTGGCTCGCA
GGGTGAGCCTGTGCGGCCACTGAGCCGGGTGGAATCCTACCTATGCCCTATGTCTACATGAGGCCACCCGAGTGC
AGCTGTGCTGCCACTCTGTGTGCTGAAGCTGTGTCAGCCCCGGCTTTCCTCGAGGCGTTTGGCAGCCAATGCTCC
TGGAGCCAGGAACATGCAATTGCTCACCTGTTGCTGGTCTACGGGCACAGAGAAGGTGGCCGTGGAGCTCCAG
ACCAATTTCTTGGSGTGAAGCTCGACAGCGGAGTTAGAGCGAGGTTACCCTGGGACGAGGCTGGCCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGAGCGTGGTCTCGAAGAAGCACCTGTGGACACTCTCT
TCTTCTTACACCGCTGTGGACAAGGCTGGGCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
GGCAGGCTCTTTTCAGTCCATTTCCAGGAGTTCAACTCTGCCCTGTACACAGAGATACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTTCTGTTGTGACCCCTCCCGGGGGGCTCCTATAGGGGGGAGATTG
ACCGGCGAGCTTCTGCGGAGGGCTGTCTTCAACCGCTGACTACTGGCGGCCGAGCCCGCTGGCAGGTGAAC
TGCACGCTCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGTGATGATGTTTTCCTCCGTTCTCAGGGCTCC
ACCTCTTTCCGGGCTGAGGCGAGGCGCTGGTGACAGAAGTTCTCCCTGCGAGACTGAGCCACGCTCAGCTGAAG
AATCTTACACCGCTGCCGCTCAGCAACCTGGAGGGGCTAGGGGGGCTGCCACGCTGGCTTGGCTCTCTTTG
AGCAGGACAGGCCAATAGCACTTAGCCCCCTGGGGGCCCTAACCTCACTACCTTTCTTTGCTCTGCTCAGCC
CCAGGAAGGCGAAGGACAGATGGTGACAGATAGAGAATTTGTTGCTGTATTTTTAAATATGAAATGTTATTAA
ACATGTCTTCTGCC

0905348-071301

FIGURE 118

MRLSSLLALLRPALEPLILGLSLGCSLSLLRVSWIQEGEGEDPCVEAVGERGGPQNPDSSRARLD
QSDQDFKPRIVPYRDPNPKYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRVT
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDWEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALEQLNRRYQPRLRFOKQRLNGYR
RFDPARGMEYTLDLLLECVTQRGHRRALARRVSLRLPLSRVEILPMPYVTEATRVQLVLPPL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFPP
VHFQEFNPALSPQRSPPGPPGAGDPFPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLA
RARLAGELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPLGVQKFSRLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

0305348-071301

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGGGCTGCGCTTTCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAAATGTTAAAGTGTGTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTGCGAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGCGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCCTCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAATTGTTGGGCACTGGTATAACACACATTAAAG
TCAGTAGTACATTTTTAAATGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTGGAAGAAGTGTTTTAAGAATAATAATTTGCAAATAAACTATTAATAAATATTTATAT
GTGATAAATCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGATTTGGTT
AAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCTTCTCAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

000546.07304

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFN
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHI FNDALVFL
PFGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

[illegible][illegible]

FIGURE 122

MNSSKSSETQCTERGCFFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNC SAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTP LTKSL SFWDVGE PNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTFVVQEFESVELSCIITDSQTS
PRIWEKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPCRVKAVFVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEBGFHRKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267